



1 ATGTGGAAATGGATACTGACACATTGTGCCTCAGCCTTTCCCCACCTGCCCGGCTGCTGC 60
-----+-----+-----+-----+-----+-----+
TACACCTTTACCTATGACTGTGTAAACACGGAGTCGGAAGGGGTGGACGGGCCGACGACG
M W K W I L T H C A S A F P H L P G C C

61 TGCTGCTGCTTTTTGTTGCTGTTCTTGGTGTCTTCCGTCCCTGTCACCTGCCAAGCCCTT 120
-----+-----+-----+-----+-----+-----+
ACGACGACGAAAAACAACGACAAGAACCACAGAAGGCAGGGACAGTGGACGGTTCGGGAA
C C C F L L L F L V S S V P V T C Q A L

121 GGTCAGGACATGGTGTCAACAGAGGCCACCAACTCTTCTTCCTCCTCCTTCTCCTCTCCT 180
-----+-----+-----+-----+-----+-----+
CCAGTCCTGTACCACAGTGGTCTCCGGTGGTTGAGAAGAAGGAGGAGGAAGAGGAGAGGA
G Q D M V S P E A T N S S S S S F S S P

181 TCCAGCGCGGGAAGGCATGTgCGGAGCTACAATCACCTTCAAGGAGATGTCCGCTGGAGA 240
-----+-----+-----+-----+-----+-----+
AGGTCGCGCCCTTCCGTACAcGCCTCGATGTTAGTGGAAGTTCCTCTACAGGCGACCTCT
S S A G R H V R S Y N H L Q G D V R W R

MATCH WITH FIG. 1B

FIG.1A

MATCH WITH FIG. 1A

241	AAGCTATTCTCTTTCACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGGTCAGCGGG -----+-----+-----+-----+-----+-----+-----+ TTCGATAAGAGAAAGTGGTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCCC	300
	K L F S F T K Y F L K I E K N G K V S G	
301	ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT -----+-----+-----+-----+-----+-----+-----+ TGGTTCTTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA	360
	T K K E N C P Y S I L E I T S V E I G V	
361	GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC -----+-----+-----+-----+-----+-----+-----+ CAACGGCAGTTTTCGGTAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAG	420
	V A V K A I N S N Y Y L A M N K K G K L	
421	TATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA -----+-----+-----+-----+-----+-----+-----+ ATACCGAGTTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT	480
	Y G S K E F N N D C K L K E R I E E N G	

MATCH WITH FIG. 1C

FIG.1B

MATCH WITH FIG. 1B

```

481  TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG
-----+-----+-----+-----+-----+-----+-----+
ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATACACCGTAAC
      Y  N  T  Y  A  S  F  N  W  Q  H  N  G  R  Q  M  Y  V  A  L

AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC
541  -----+-----+-----+-----+-----+-----+-----+
TTACCTTTTCCTCGAGGTTCTCTCCTGTCTTTTGTGCTTCCTTTTGTGGAGACGAGTG
      N  G  K  G  A  P  R  R  G  Q  K  T  R  R  K  N  T  S  A  H

TTTCTTCCAATGGTGGTACACTCATAG
601  -----+-----+-----+-----+-----+-----+-----+
AAAGAAGGTTACCACCATGTGAGTATC
      F  L  P  M  V  V  H  S  *

```

FIG.1C

	1					50
FGF4	MS.GPGTAAV	ALLPAVLLAL	LA.....	.PWAGRGGAA	APTAPNGTLE	
FGF6	MSRGAGRLQG	TLWALVFLGI	LV.....	.GMVVPSAG	TR.ANNTLLD	
FGF5MSL	SFLLLLFFSH	LILSAWAHGE	KRLAPKGQPG	PAATDRNPIG	
FGF1	
FGF2	
FGF9MAPLGEVG	NYFGVQDAVP	
FGF7MHKW	ILTWILPTLLYRSCF	HIICLVGTIS	
KGF2MWKW	ILTHCASAFP	HLPGCCCCCF	LLLFLVSSVP	
FGF3MGL	IWLLLLSLLE	
FGF8	MGSPRSALSC	LLLHLLVLCL	QAQVRSAAQK	RGPGAGNPAD	TLGQGHEDRP	

	51					100
FGF4	AELERRWESL	VALSLARLPV	AA..QPKEAA	VQSGAGDY..	...LLGIKRL	
FGF6	S...RGWGTL	LSRSRAGLAG	EI.....AG	VNWESG.Y..	...LVGIKRQ	
FGF5	SSSRQSSSSA	MSSSSASSSP	AASLGSQGS	LEQSSFQW..	...SPSGRRT	
FGF1MAEG	EITTF TALTE	KFN...LPPGN..	...YK...KP	
FGF2MAAG	SITTLPALPE	DGGSGAFPPGH..	...FK...DP	
FGF9	FGNVPVLPVD	SPVLLSDHLG	QSEAGGLPRG	PAVTDLDH..	...LKGILRR	
FGF7	LACNDMTPEQ	M...ATNVNCSSPE	RHTRSVDY..	...MEGGDIR	
KGF2	VTCQALGQDM	VSPEATNSSS	SSFSSPSSAG	RHVRSYNH..	...LQ.GDVR	
FGF3	PGWPAAGPGARLRRDAG	GRGGVYEH..	...L.GGAPR	
FGF8	FGQRSRAGKN	FTNPAPNYPE	EGSKEQRDSV	LPKVTQRHVR	EQSLVTDQLS	

MATCH WITH FIG. 2B

FIG. 2A

MATCH WITH FIG. 2A

	101		150
FGF4	RRL.....YC	NVGIGFHLQA	LPDGRIGGAH ADT.RDSLLE LSPVERGV.V
FGF6	RRL.....YC	NVGIGFHLQV	LPDGRISGTH EEN.PYSLLE ISTVERGV.V
FGF5	GSL.....YC	RVGIGFHLQI	YPDGKVNGSH EAN.MLSVLE IFAVSQGI.V
FGF1	KLL.....YC	SNG.GHFLRI	LPDGTVDGTR DRSDQHIQLQ LSAESVGE.V
FGF2	KRL.....YC	KNG.GFFLRI	HPDGRVDGVR EKSDPHIKLQ LQAEERGV.V
FGF9	RQL.....YC	R.T.GFHLEI	FPNGTIQGTR KDHSRFGILE FISIARGV.V
FGF7	VRR.....LF	CRT.QWYLRI	DKRGKVKGTQ EMKNNYNIME IRTVAVGI.V
KGF2	WRK.....LF	SFT.KYFLKI	EKNGKVS GTK KENC PYSILE ITSVEIGV.V
FGF3	RRK.....LY	CAT.KYHLQL	HPSGRVNGSL .ENSAYSILE ITAVEVGI.V
FGF8	RRLIRTYQLY	SRTSGKHVQV	LANKRINAMA EDGDPFAKLI VETDTFGSRV

	151		200
FGF4	SIFGVASRFF	VAMSSKGKLY	G.SPFFTDEC TFKEILLPNN YNAYESYKYP
FGF6	SLFGVRSALF	VAMNSKGRLY	A.TPSFQEEC KFRETLLPNN YNAYESDLYQ
FGF5	GIRGVFSNKF	LAMSKKGKLY	A.SAKFTDDC KFRERFQENS YNTYASAIHR
FGF1	YIKSTETGQY	LAMDTDGLLY	G.SQTPNEEC LFLEERLEENH YNTYISKKH.
FGF2	SIKGVCANRY	LAMKEDGRL	A.SKCVTDEC FFFERLESNN YNTYRSRKY.
FGF9	SIRGVDSGLY	LGMNEKGELY	G.SEKLTQEC VFREQFEENW YNTYSSNLYK
FGF7	AIKGVESSEFY	LAMNKEGKLY	A.KKECNEDC NFKELILENH YNTYAS....
KGF2	AVKAINSNNY	LAMNKKGKLY	G.SKEFNNDK KLKERIEENG YNTYAS....
FGF3	AIRGLFSGRY	LAMNKRGRLY	A.SEHYSAEC EFVERIHELG YNTYASRLYR
FGF8	RVRGAETGLY	ICMNKKGKLI	AKSNGKGKDC VFTEIVLENN YTALQNAKY.

MATCH WITH FIG. 2C

FIG. 2B

MATCH WITH FIG. 2B

	201		250
FGF4	GM.....FI	ALSKNGKTKK G..NRVSPTM KVTHFLPRL.
FGF6	GT.....YI	ALSKYGRVKR G..SKVSPIM TVTHFLPRI.
FGF5	TEKTGREWYV	ALNKRKAKR GCSPRVKPQH ISTHFLPRFK
FGF1AEKNWFV	GLKNGSCKR G..PRTHYGQ KAILFLPLPV
FGF2T..SWYV	ALKRTGQYKL G..SKTGPGQ KAILFLPMSA
FGF9	HV.....	..DTGRRYYV	ALNKDGTPRE G..TRTKRHQ KFTHFLPRPV
FGF7	AKW THNGGEM.FV	ALNQKGIPVR G..KKTKEQ KTAHFLPMAI
KGF2	FNW QHNGRQM.YV	ALNGKGAPRR G..QKTRRKN TSAHFLPMVV
FGF3	TVSSTPGARR	QPSAERLWYV	SVNGKGRPRR G..FKTRRTQ KSSLFLPRVL
FGF8EGWYM	AFTRKGRPRK G..SKTRQHQ REVHFMKRLP

	251		300
FGF4
FGF6
FGF5	QSEQPELSFT	VTVPKKNPP	SPIKSKIPLS APRKNTNSVK YRLKFRFG..
FGF1	SSD.....
FGF2	KS.....
FGF9	DPDKVPELYK	DILSQS....
FGF7	T.....
KGF2	HS.....
FGF3	DHRDHEMVRQ	LQSGLP RPPG	KGVP RRRRQ KQSPDNLEPS HVQASRLGSQ
FGF8	RGHHTTEQSL	RFEFLNYPPF	TRSLRGSQRT WAPEPR....

MATCH WITH FIG. 2D

FIG. 2C

MATCH WITH FIG. 2C

	301
FGF4
FGF6
FGF5
FGF1
FGF2
FGF9
FGF7
<i>KGF2</i>
FGF3	LEASAH
FGF8

FIG.2D

GGAATTCCGG GAAGAGAGGG AAGAAAACAA CGGCGACTGG GCAGCTGCCT CCACTTCTGA	60
CAACTCCAAA GGGATATACT TGTAAGAGTG GCTCGCAGGC TGGGGCTCCG CAGAGAGAGA	120
CCAGAAGGTG CCAACCGCAG AGGGGTGCAG ATATCTCCCC CTATTCCCCA CCCCACCTCC	180
CTTGGGTTTT GTTCACCGTG CTGTCATCTG TTTTTCAGAC CTTTTTGGCA TCTAACATGG	240
TGAAGAAAGG AGTAAAGAAG AGAACAAAGT AACTCCTGGG GGAGCGAAGA GCGCTGGTGA	300
CCAACACCAC CAACGCCACC ACCAGCTCCT GCTGCTGCGG CCACCCACGT CCACCATTTA	360
CCGGGAGGCT CCAGAGGCGT AGGCAGCGGA TCCGAGAAAG GAGCGAGGGG AGTCAGCCGG	420
CTTTTCCGAG GAGTTATGGA TGTTGGTGCA TTCACTTCTG GCCAGATCCG CGCCAGAGG	480
GAGCTAACCA GCAGCCACCA CCTCGAGCTC TCTCCTTGCC TTGCATCGGG TCTTACCCTT	540
CCAGTATGTT CCTTCTGATG AGACAATTTC CAGTGCCGAG AGTTTCAGTA CA ATG Met	595
TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG CCC	643
Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro	
GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC GTC	691
Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val	
CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG GCC	739
Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala	
ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA AGG	787
Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg	
CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA AAG	835
His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys	
CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG AAG	883
Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys	
GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA	931
Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile	
ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC	979
Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn	
TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA	1027
Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu	
TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC	1075
Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr	

FIG.3A

AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT	1123
Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr	
GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA	1171
Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg	
AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	1216
Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG	1276
GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC	1336
TTAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCAC TGACATATG ATGTTCTTTT	1396
AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT	1456
ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTGTGTGT TGTGTCAAG TTTTGTTTT	1516
TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG	1576
GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT	1636
GAATCAATGA ACAGTAATAC GTGCAAGCAT TTA CTGGAAA GCACTTGGGT CATATCATAT	1696
GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTAAAAATA	1756
TAAACATGTT AGTGTGAAAC TGTCTAACA ATACAAATAG TATGGTATGC TTGTGCATTC	1816
TGCCTTCATC CCTTTCTATT TCTTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT	1876
TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG	1936
CACACCACAT GCATGTTTAC GACAAAGTGT TTTTAAACT TGGCGAACAC TTCAAAAATA	1996
GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA	2056
CTTCTGCAGT AATAACCATC AACAATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG	2116
AGATGTCTGC TATCATTTGA AAACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA	2176
GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA	2236
AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT	2296
TTCTTGCCAA ATGTCATGGC GGTAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA	2356
TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT	2416

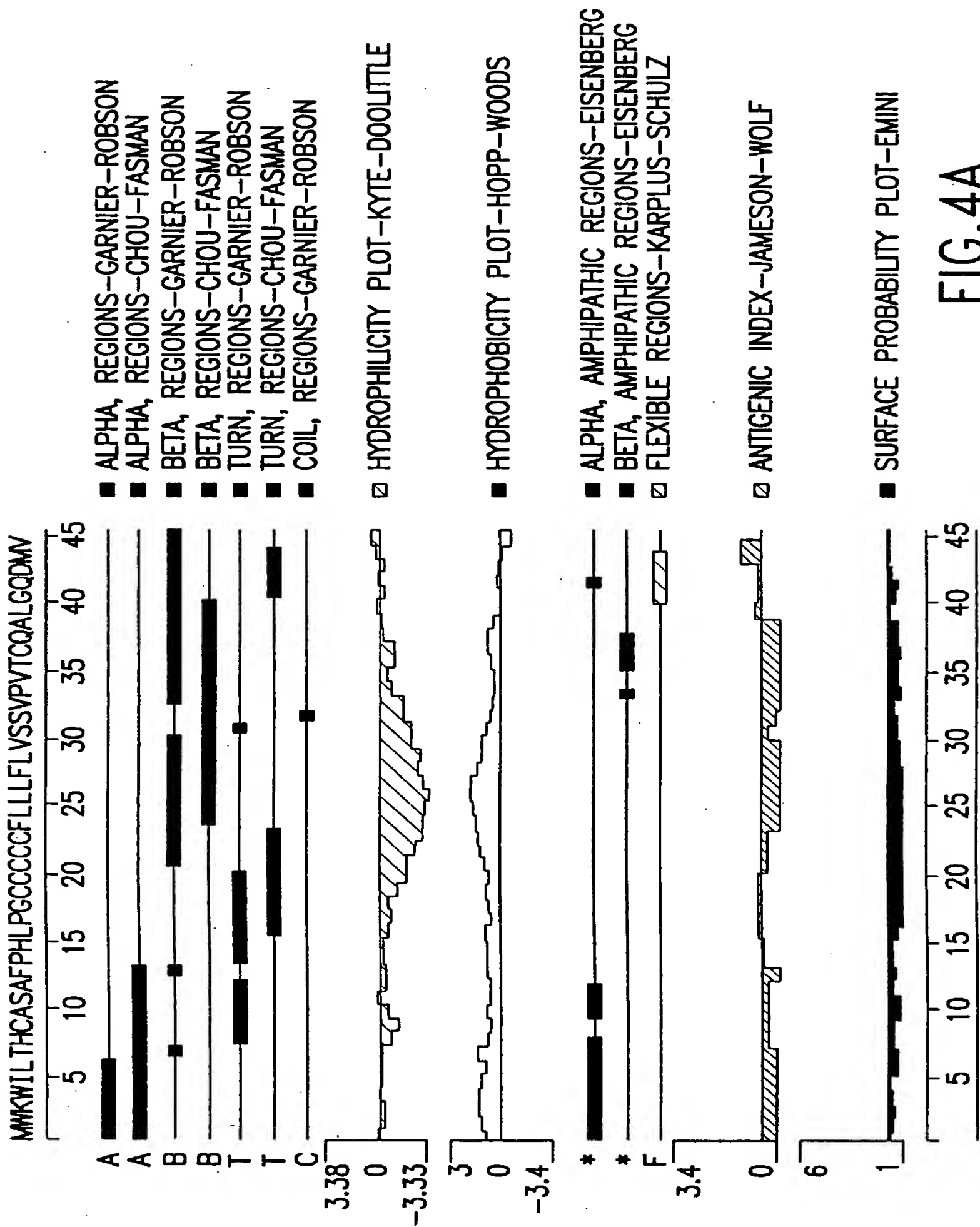
FIG.3B

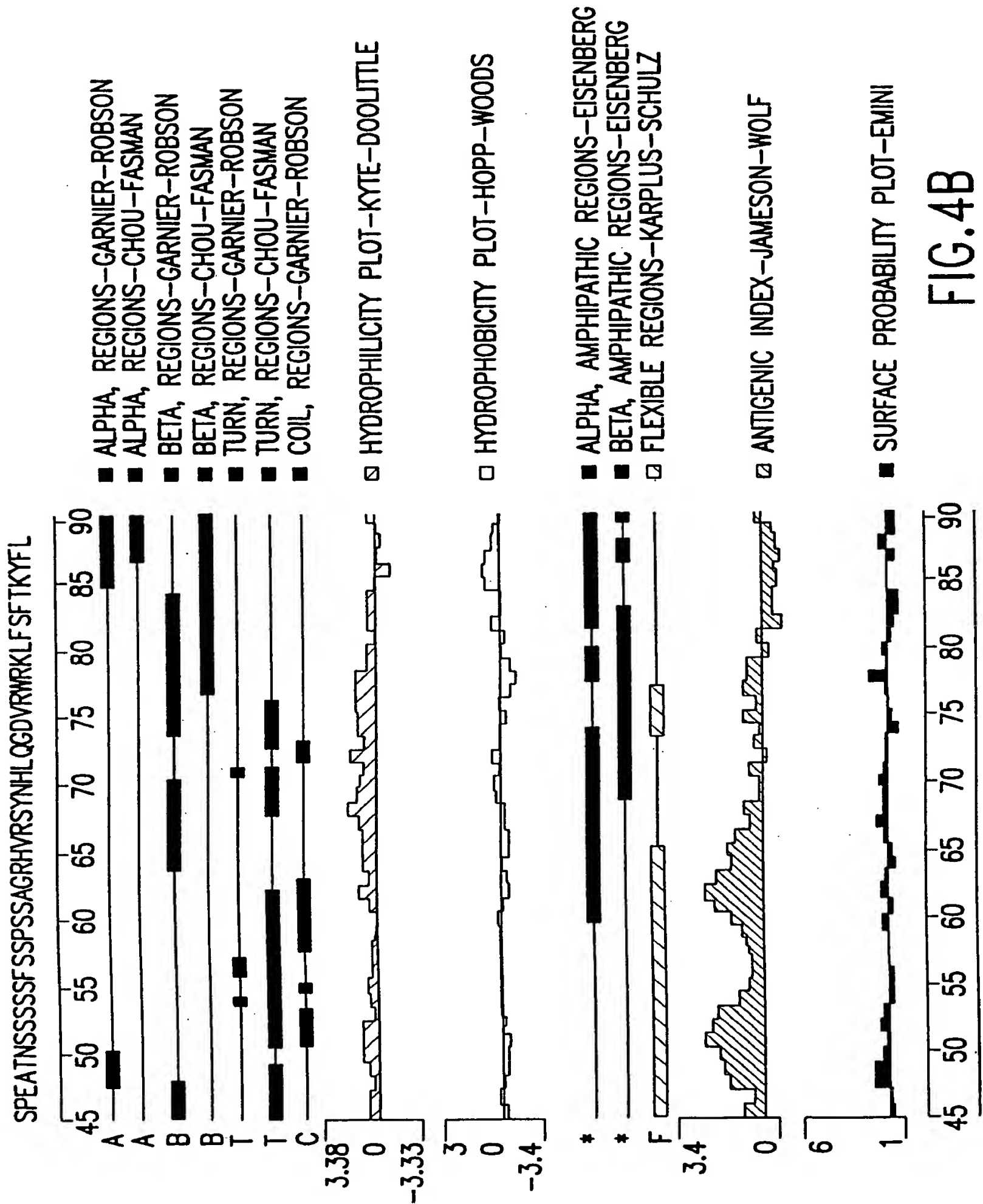
CCCAGGGGCT	TAAACTGAGC	AAATCAAATA	TATACTGGTA	TATGTGTAAC	CATATACAAA	2476
AACCTGTTCT	AGCTGTATGA	TCTAGTCTTT	ACAAAACCAA	ATAAACTTG	TTTTCTGTAA	2536
ATTTAAAGAG	CTTTACAAGG	TTCCATAATG	TAACCATATC	AAAATTCATT	TTGTTAGAGC	2596
ACGTATAGAA	AAGAGTACAT	AAGAGTTTAC	CAATCATCAT	CACATTGTAT	TCCACTAAAT	2656
AAATACATAA	GCCTTATTTG	CAGTGTCTGT	AGTGATTTTA	AAAATGTAGA	AAAATACTAT	2716
TTGTTCTAAA	TACTTTTAAG	CAATAACTAT	AATAGTATAT	TGATGCTGCA	GTTTTATCTT	2776
CATATTTCTT	GTTTTGAAAA	AGCATTTTAT	TGTTTGGACA	CAGTATTTTG	GTACAAAAAA	2836
AAAGACTCAC	TAAATGTGTC	TTACTAAAGT	TTAACCTTTG	GAAATGCTGG	CGTTCTGTGA	2896
TTCTCCAACA	AACTTATTTG	TGTCAATACT	TAACCAGCAC	TTCCAGTTAA	TCTGTTATTT	2956
TTAAAAATTG	CTTTATTAAG	AAATTTTTTG	TATAATCCCA	TAAAAGGTCA	TATTTTTCCC	3016
ATTCTTCAAA	AAAACGTAT	TTCAGAAGAA	ACACATTTGA	GGCACTGTCT	TTTGGCTTAT	3076
AGTTTAAATT	GCATTTTCATC	ATACTTTGCT	TCCAACCTGC	TTTTTGGCAA	ATGAGATTAT	3136
AAAAATGTTT	AATTTTTGTG	GTTGGAATCT	GGATGTAAA	ATTTAATTGG	TAACTCAGTC	3196
TGTGAGCTAT	AATGTAATGC	ATTCCTATCC	AACTAGGTA	TCTTTTTTTC	CTTTATGTTG	3256
AAATAATAAT	GGCACCTGAC	ACATAGACAT	AGACCACCCA	CAACCTAAAT	TAAATGTTTG	3316
GTAAGACAAA	TACACATTGG	ATGACCACAG	TAACAGCAAA	CAGGGCACAA	ACTGGATTCT	3376
TATTTACAT	AGACATTTAG	ATTACTAAAG	AGGGCTATGT	GTAAACAGTC	ATCATTATAG	3436
TACTCAAGAC	ACTAAAACAG	CTTCTAGCCA	AATATATTAA	AGCTTGCAGA	GGCCAAAAAT	3496
AGAAAACATC	TCCCCTGTCT	CTCCCACATT	TCCCTCACAG	AAAGACAAAA	AACCTGCCTG	3556
GTGCAGTAGC	TCACACCTGT	AATCCCAGCA	GTTTGGGAGA	CTGTGGGAAG	ATGGCTTGAG	3616
TCCAGGAGTT	CTAGACAGGC	CTGAGAAACC	TAGTGAGACA	TCCTTCTCTT	AAACAAAACA	3676
AAACAAAACA	AATGTAGCCA	TGCGTGGTGG	CATATACCTG	TGGTCCCAAC	TACTCAGGAG	3736
GCTGAAACGG	AAGGATCTCT	TGGGCCCCAG	GAGTTTGAGG	CTGCAGTGAG	CTATAATCTT	3796
GCCATTGCAC	TCCAGCCTGG	GTGAAAAAGA	GCCAGAAAGA	AAGGAAAGAG	AGAAAAGAGA	3856
AAAGAAAGAG	AGAAAAGACA	GAAAGACAGG	AAGGAAGGAA	GGAAGGAAGG	AAGGAAGGAA	3916
GGAAGCAAGG	AAAGAAGGAA	GGAAGGAAAG	AAGGGAGGGA	AGGAAGGAGA	GAGAAAGAAA	3976
GATTGTTTGG	TAAGGAGTAA	TGACATTCTC	TTGCATTTAA	AAGTGGCATA	TTTGCTTGAA	4036

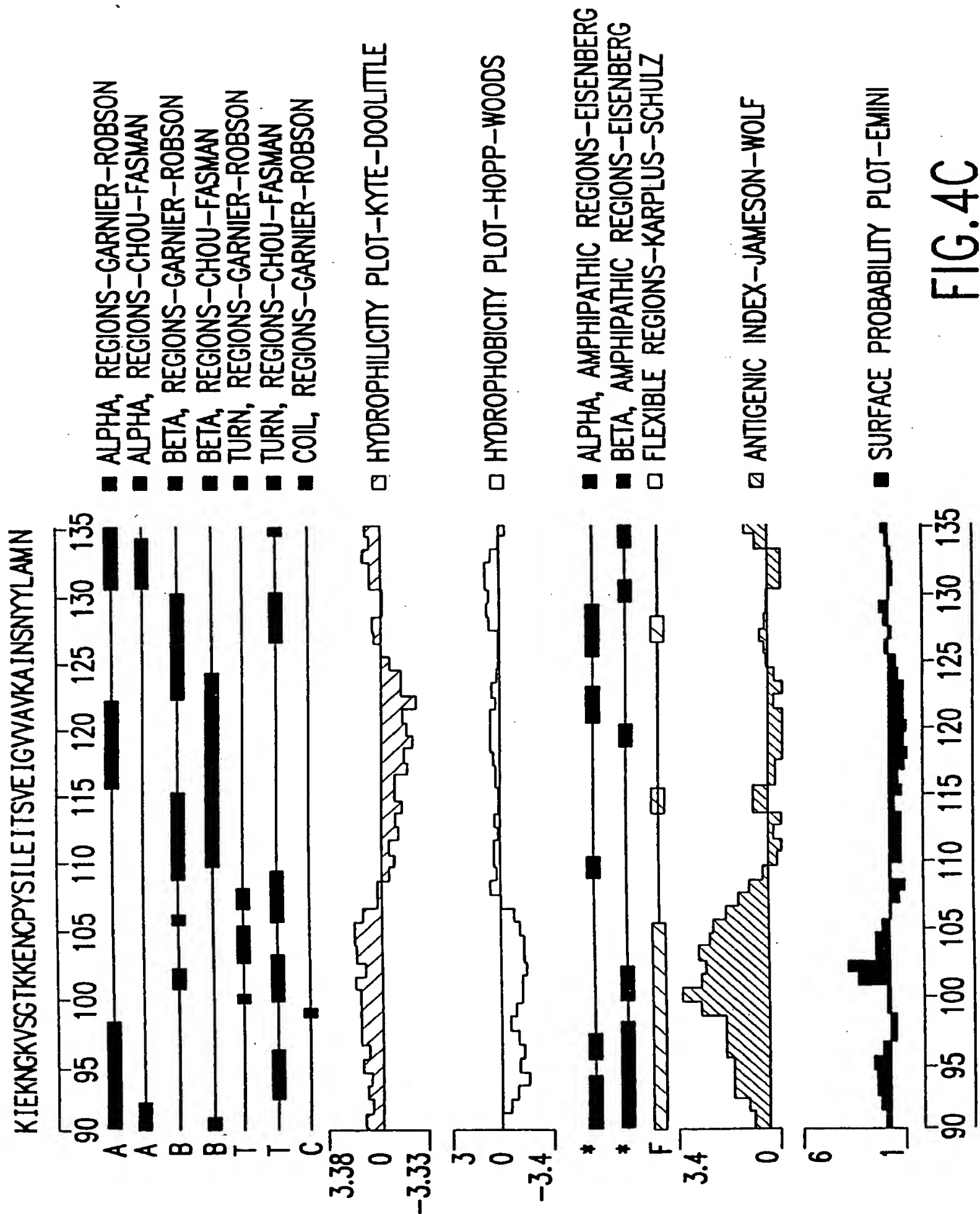
FIG.3C

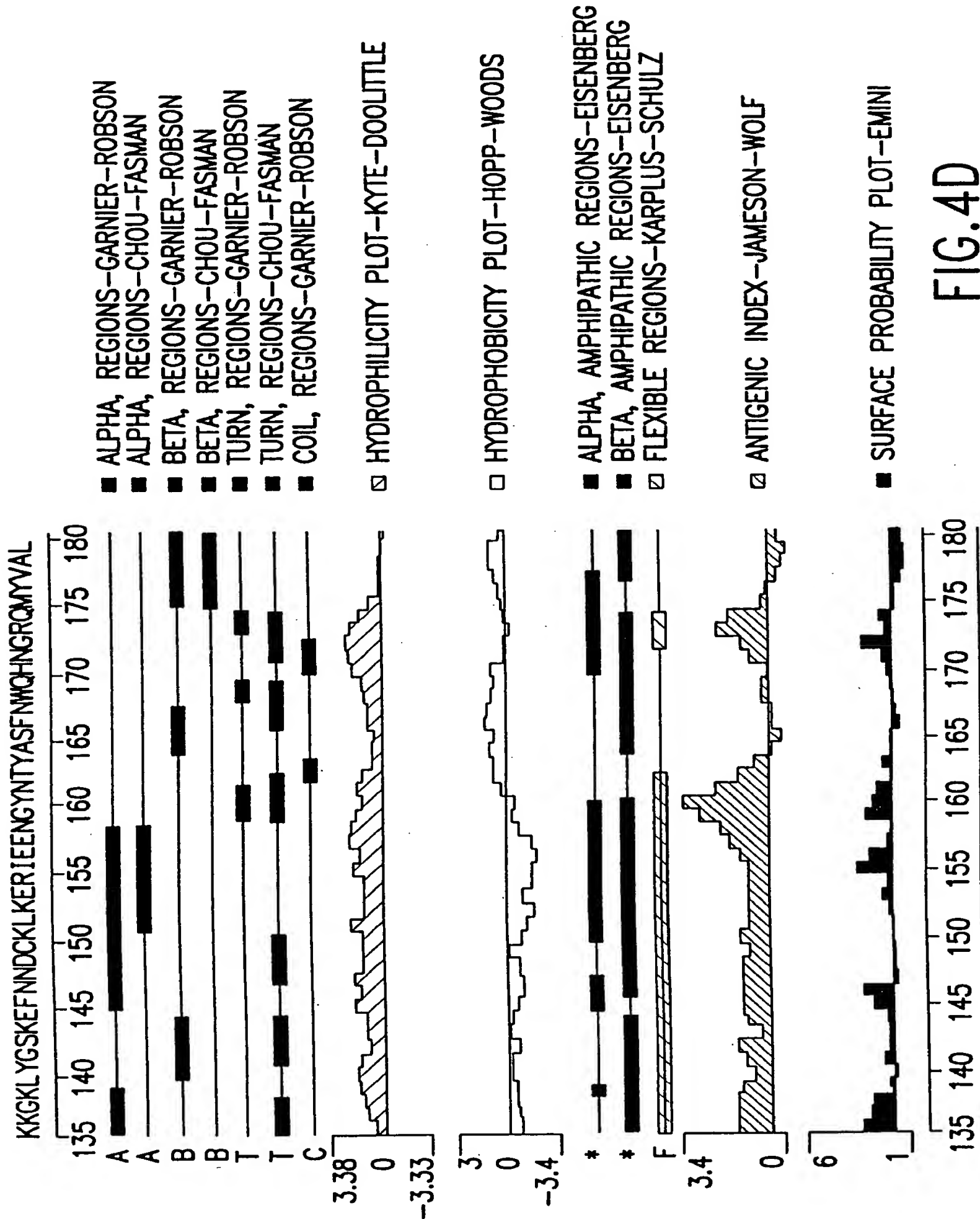
ATGGAAATAG AATTCTGGTC CCTTTTGCAA CTACTGAGA AAAAAAAAAAG CAGTTTCAGC	4096
CCTGAATGTT GTAGATTGA AAAAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA	4156
TTCGCCCTAT AGTGAGTCGT A	4177

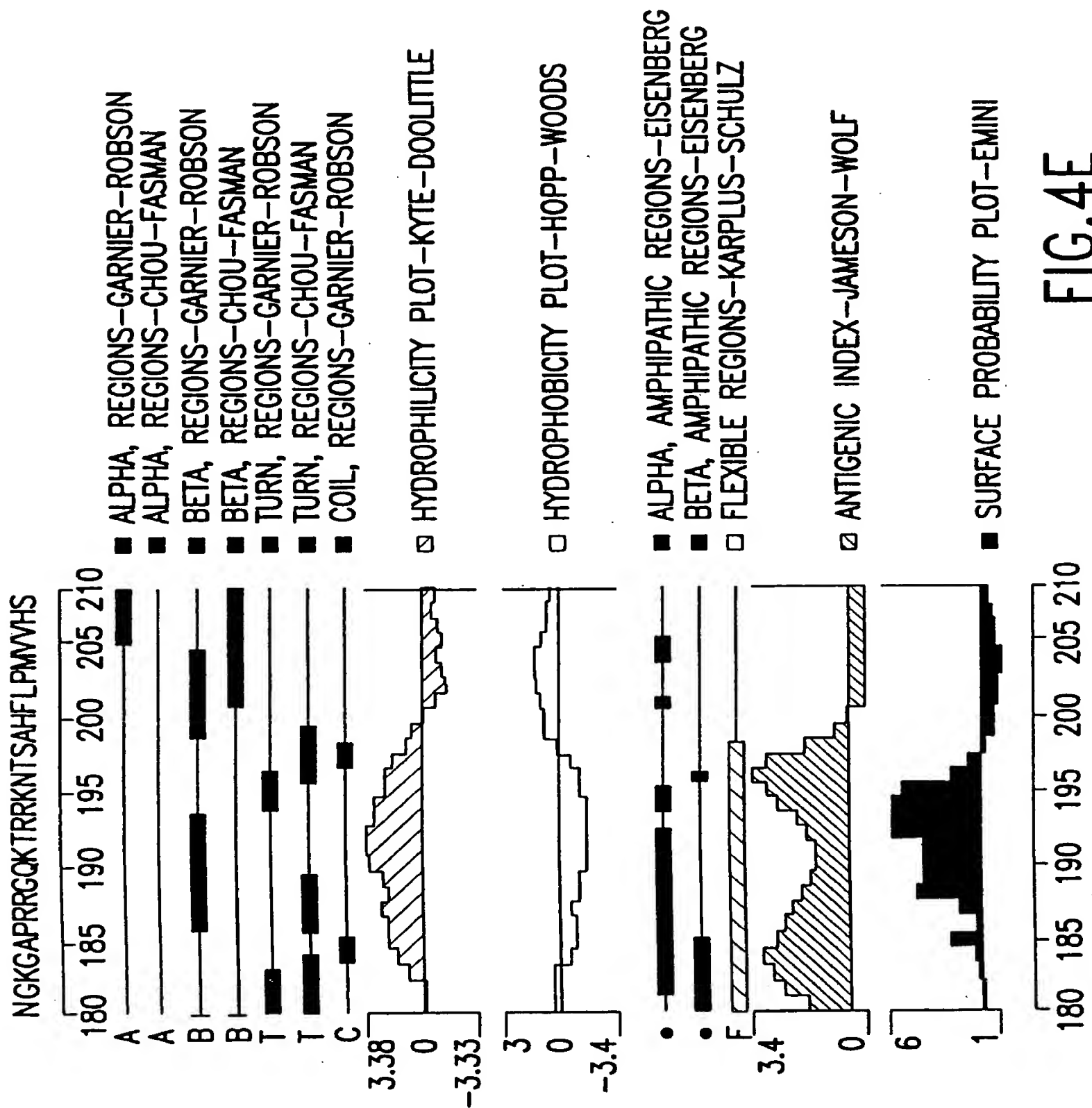
FIG.3D











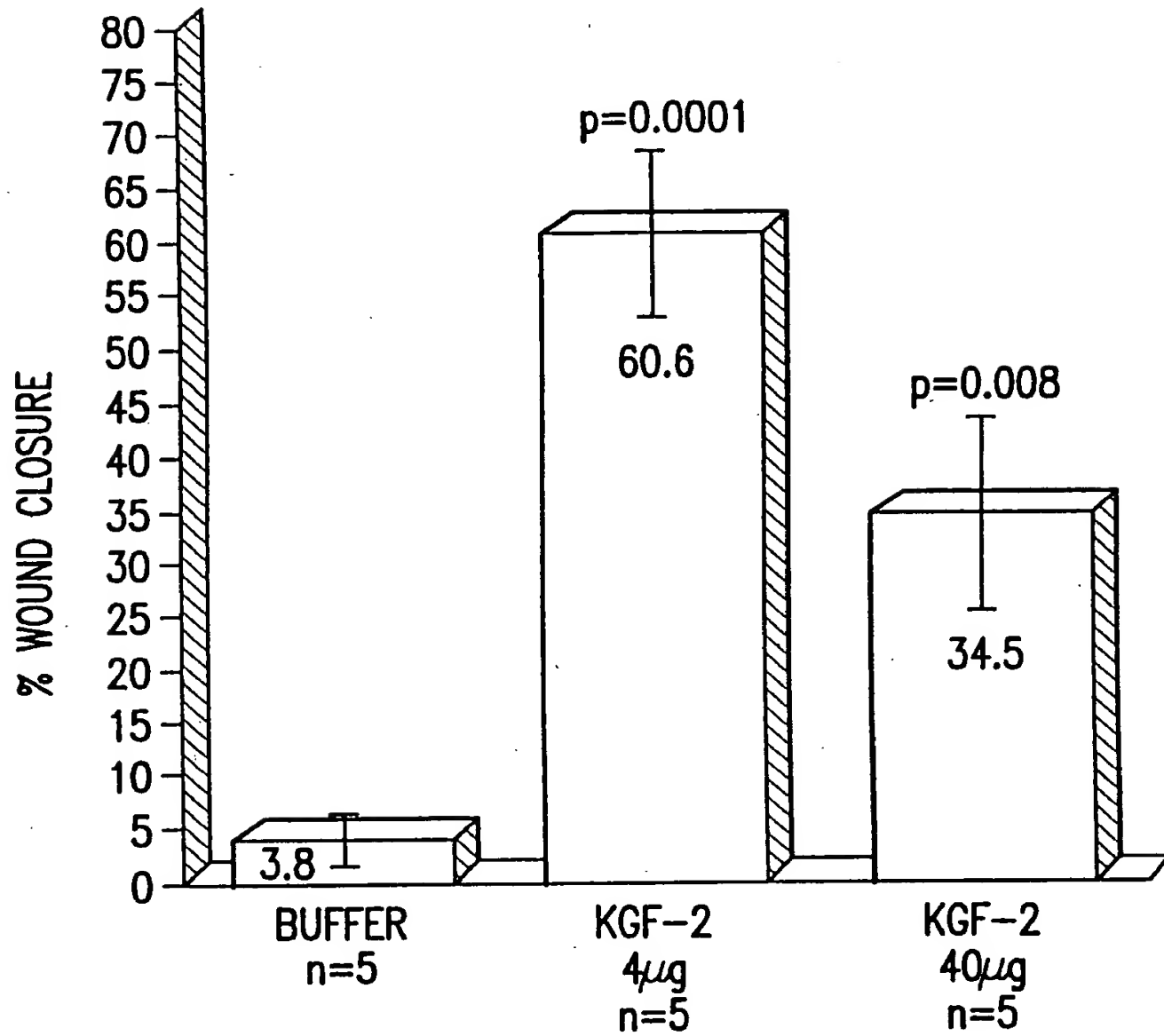


FIG.5

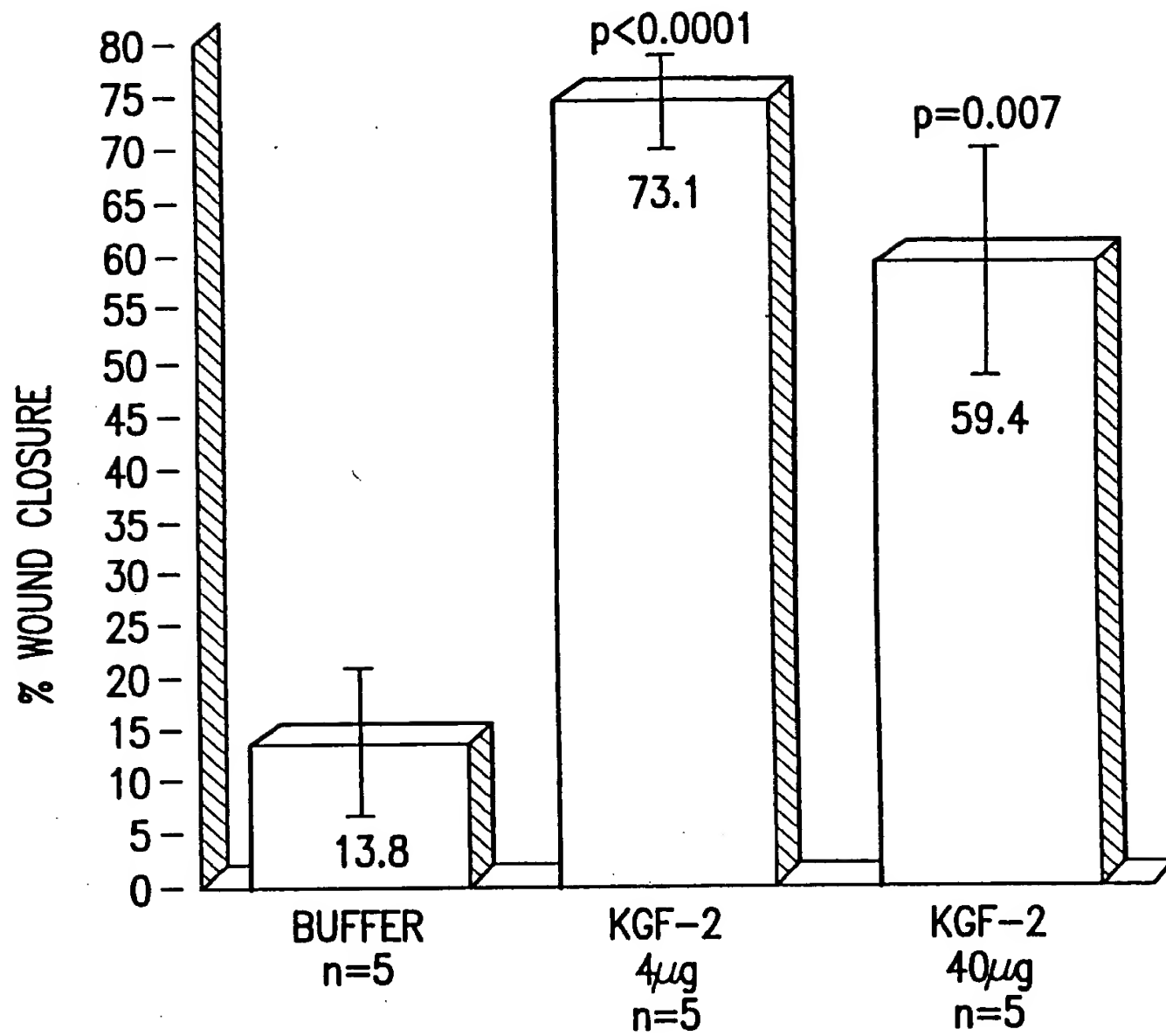


FIG.6

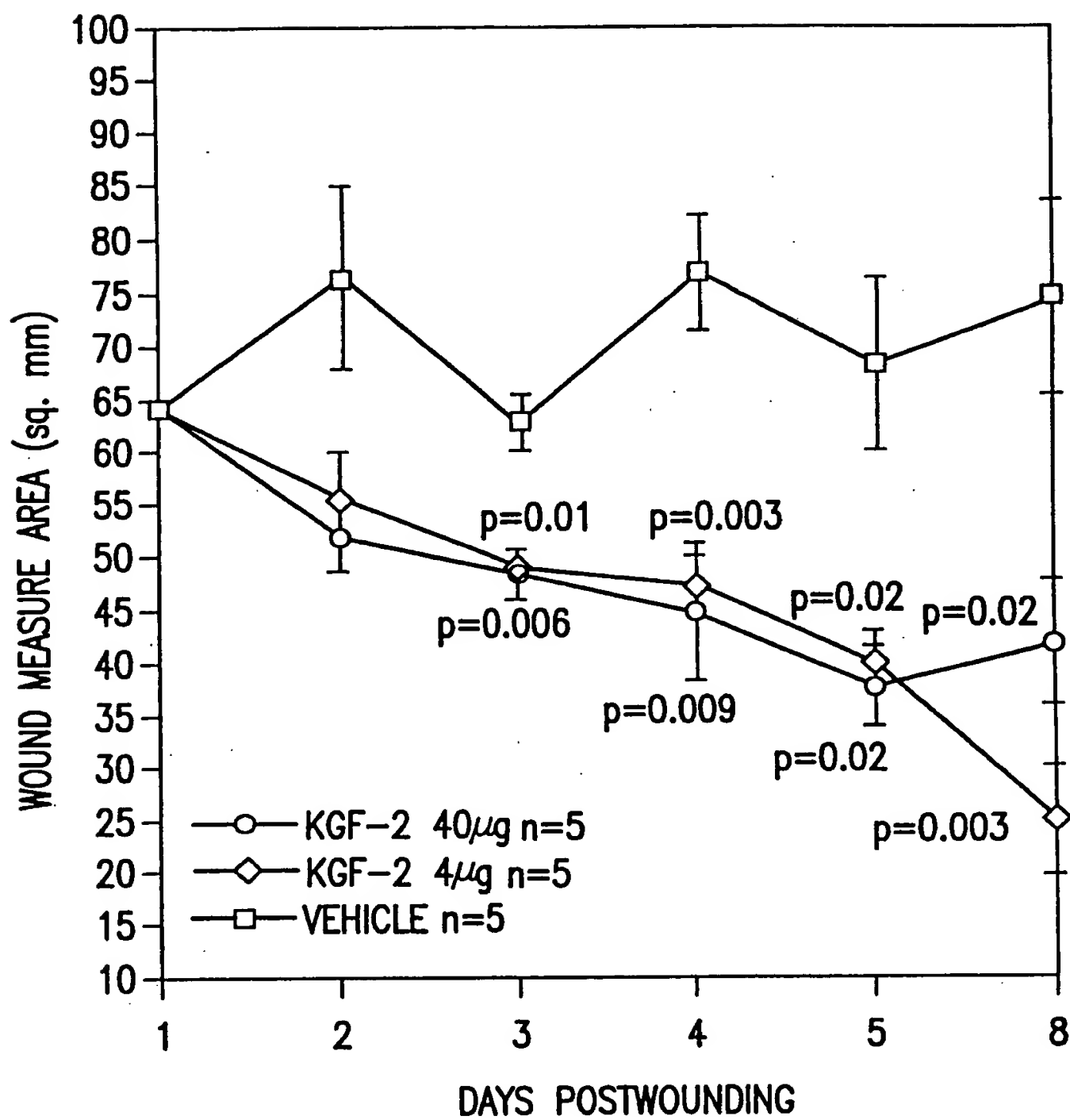


FIG.7

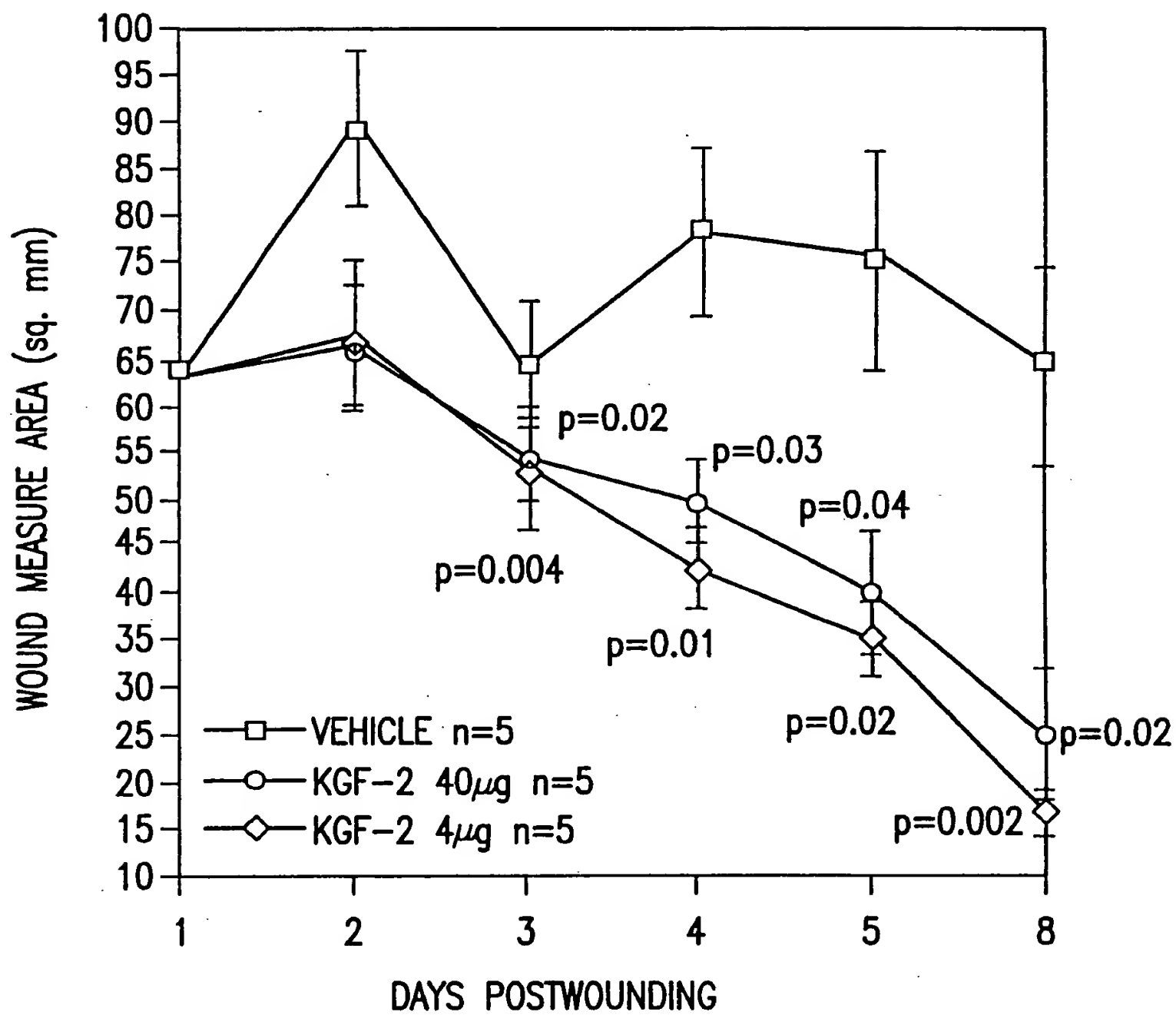
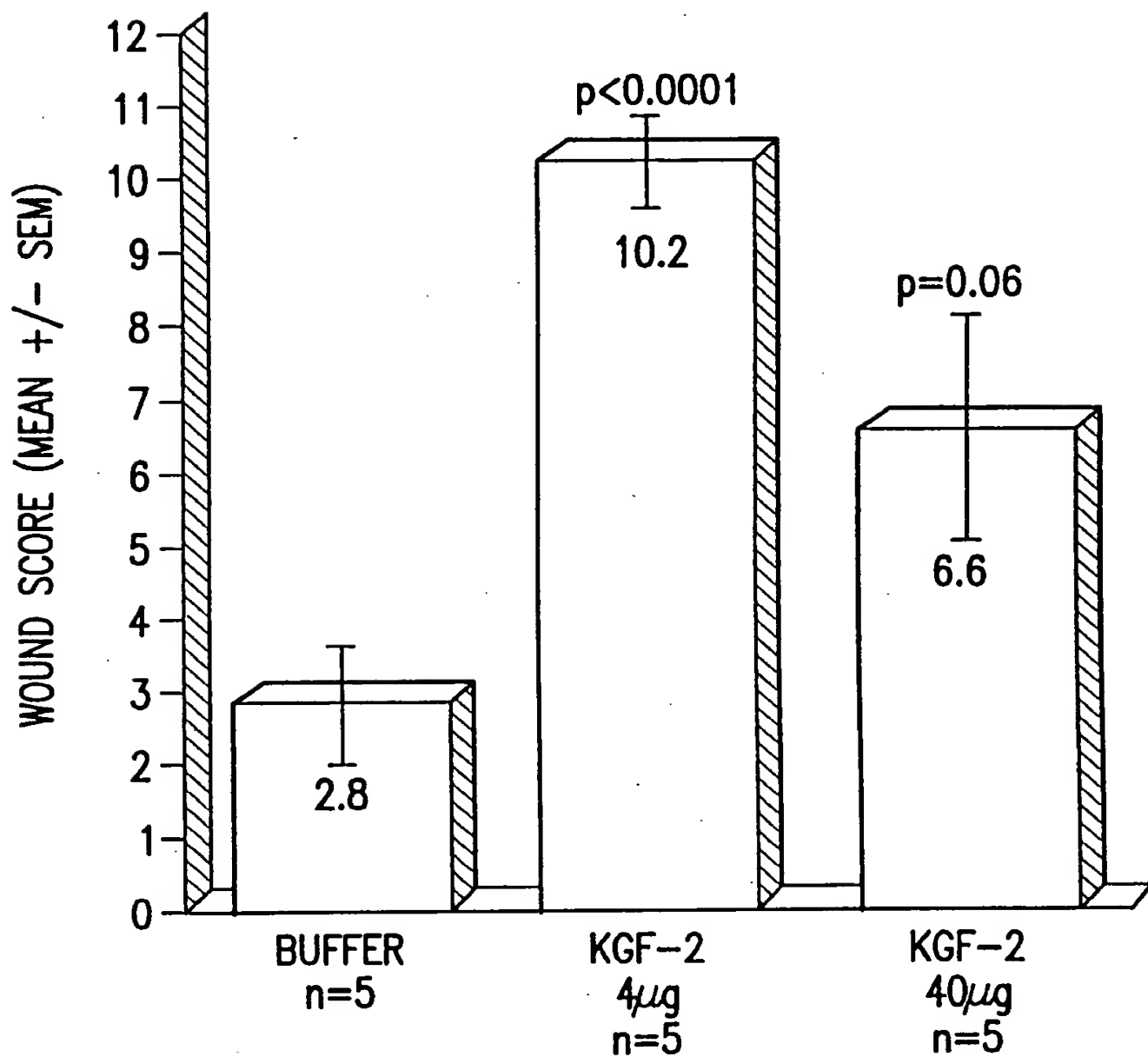
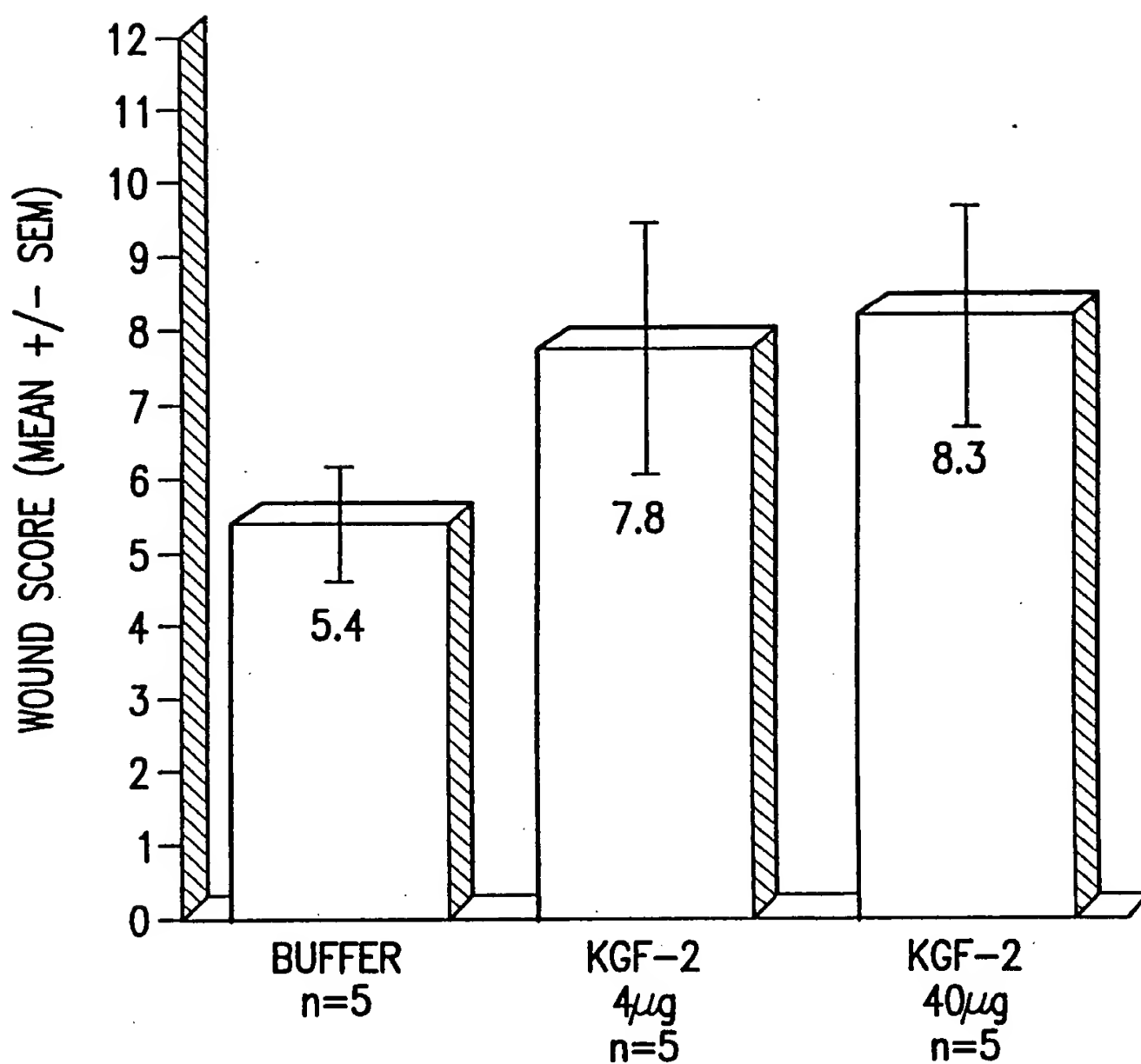


FIG.8



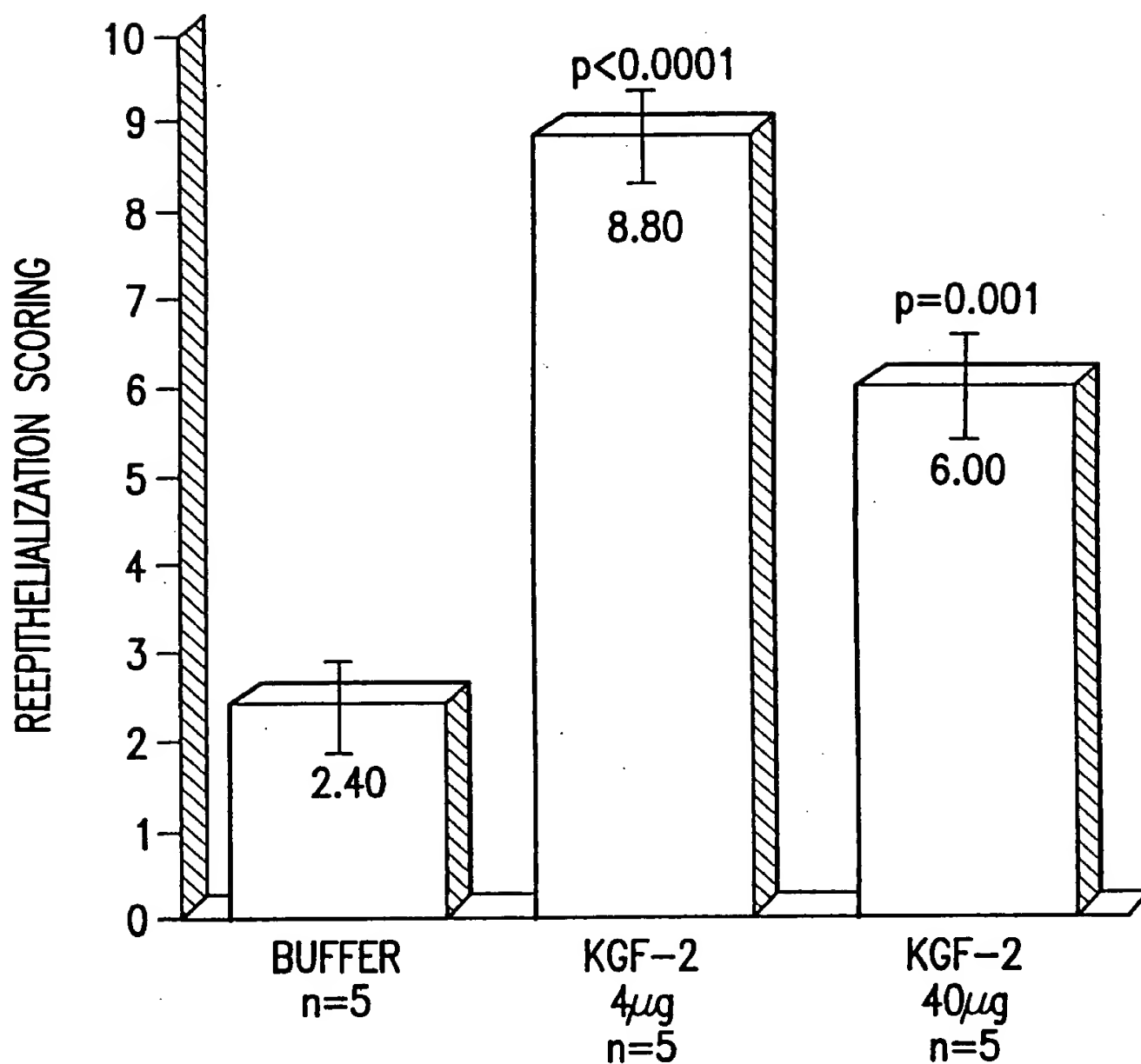
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.9



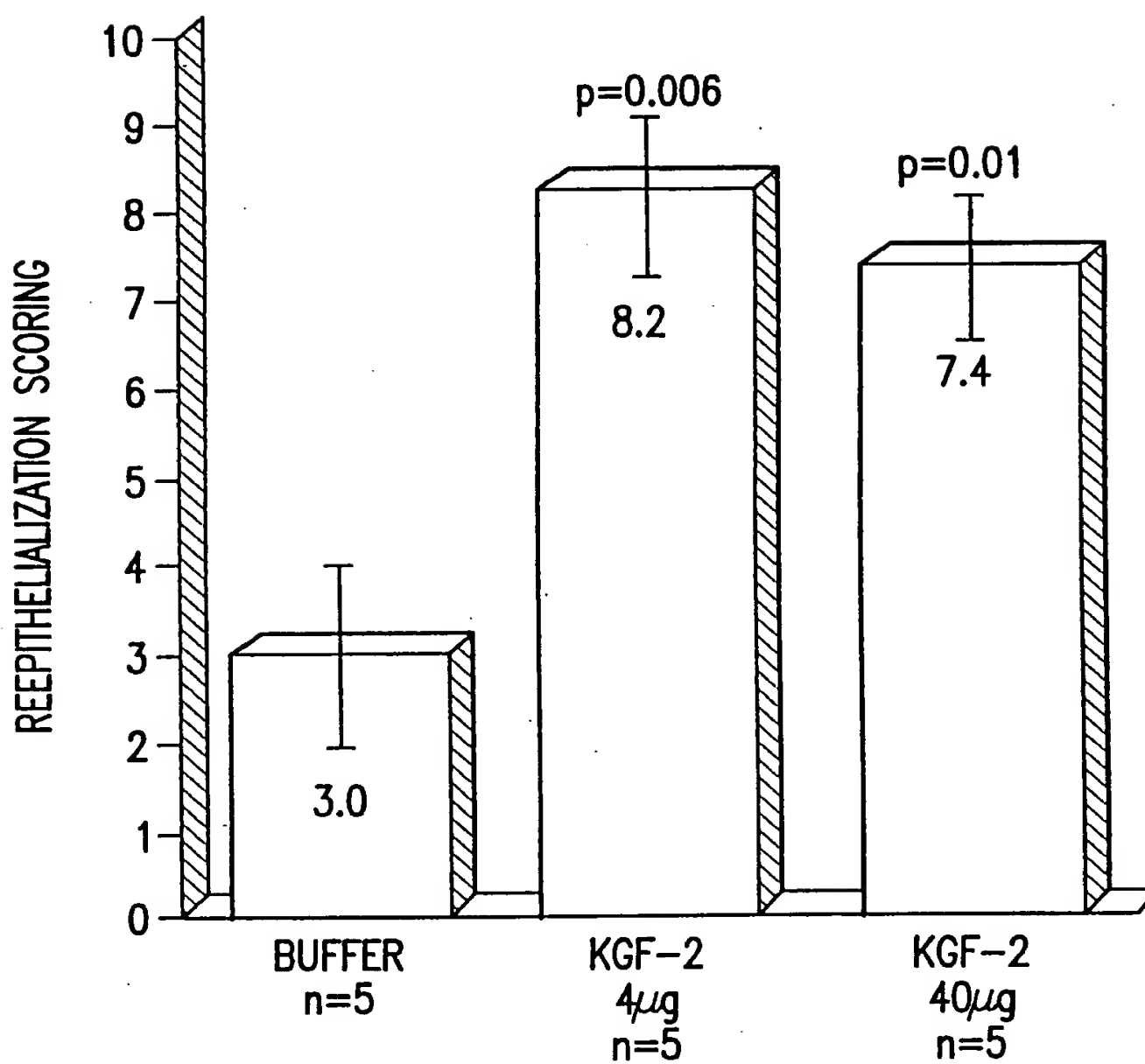
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES
7-9 GRANULATION TISSUE, CELLS, FIBROBLASTS, NEW EPITHELIUM
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.10



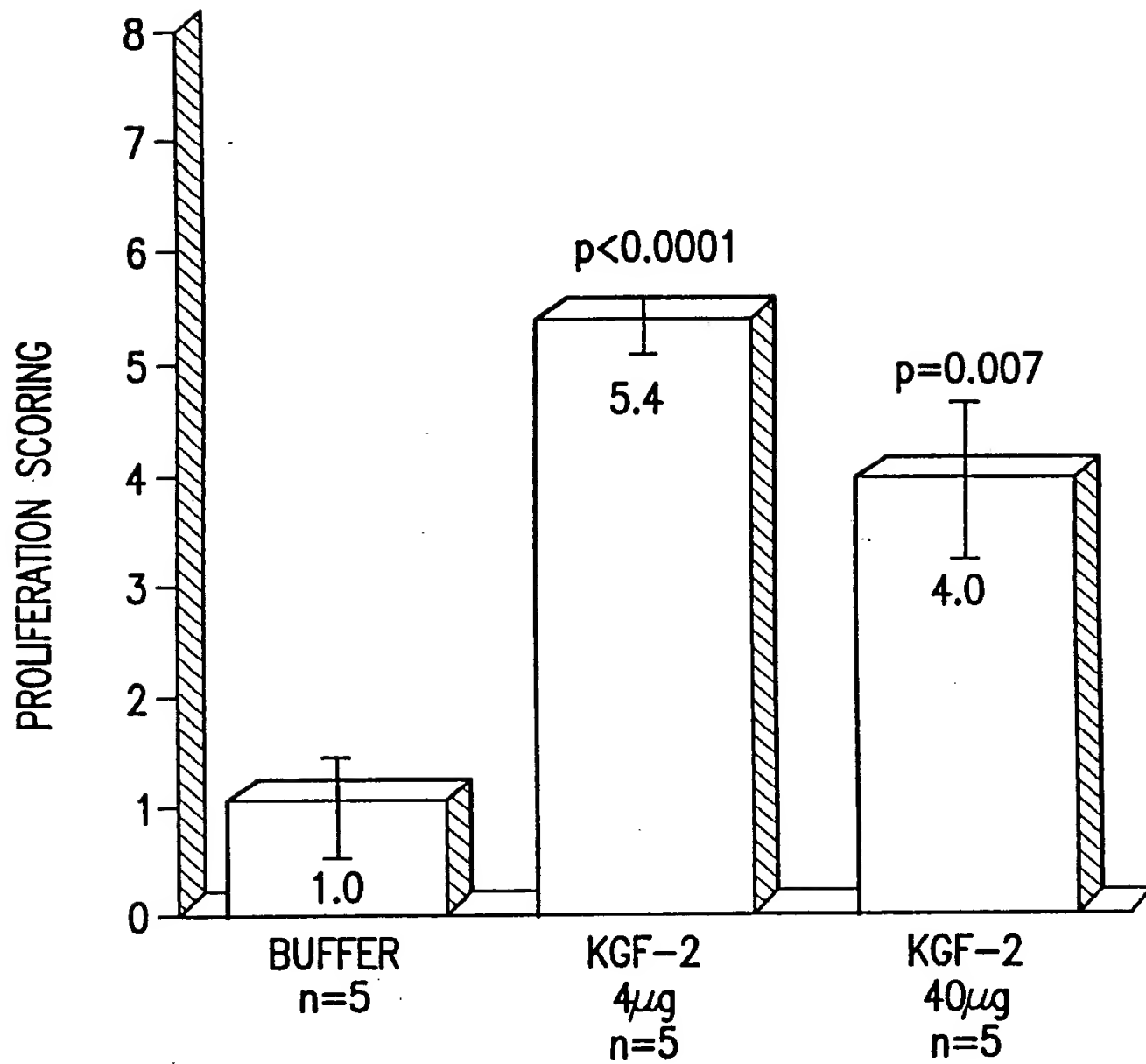
ANTI-CYTOKERATIN IMMUNOSTAINING
0-NO CLOSURE
5-SLIGHT TO MODERATE CLOSURE
10-COMPLETE CLOSURE

FIG.11



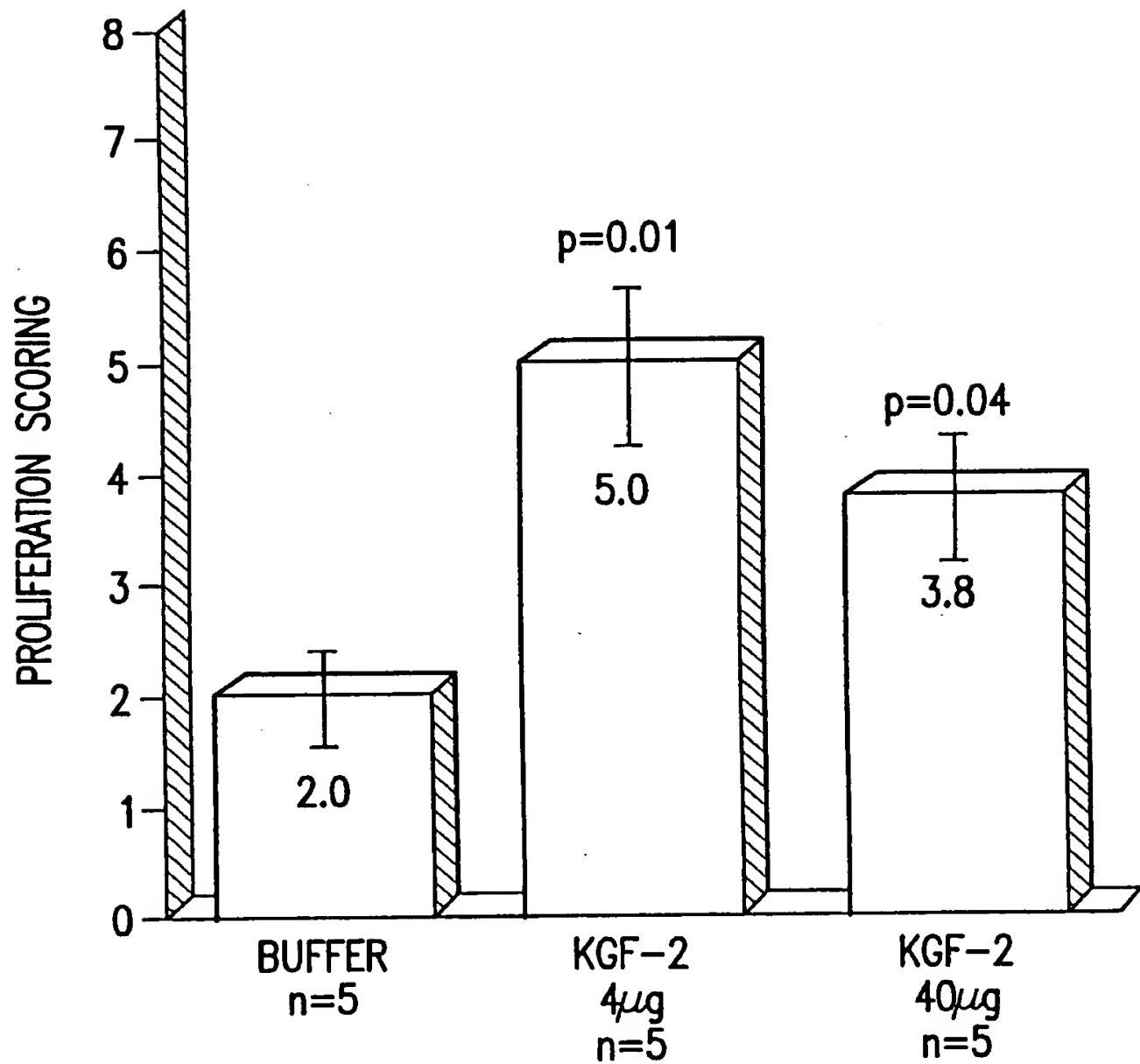
ANTI-CYTOKERATIN IMMUNOSTAINING
0-NO CLOSURE
5-SLIGHT TO MODERATE CLOSURE
10-COMPLETE CLOSURE

FIG.12



PCNA SCORING
0-2 SLIGHT PROLIFERATION
3-5 MODERATE PROLIFERATION
6-8 INTENSE PROLIFERATION

FIG.13



PCNA SCORING
0-2 SLIGHT PROLIFERATION
3-5 MODERATE PROLIFERATION
6-8 INTENSE PROLIFERATION

FIG.14

ATGAGAGGATCGCATCACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC
AGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCC
CGTCTTCCGCTGGTCGTCACGTTTCGTTCTTACAACCACCTGCAGGGTGACGTTT
GTTGGCGTAAACTGTTCTCTTTACCAAATACTTCCTGAAAATCGAAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTG
GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAG
CAACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAG
AATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT
ACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGA_dTGGAAAAGGAGCTCCA_dGGAGAGGACAGAAAACACGAAG
GAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MRGSHHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD
VRWRKLFSTKYFLKIEKNGKVSGTKKENCPSILEITSVEIGVVAVKAINSN
YYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS

kgf-2 synthetic cys37 Bam HI
AAAGGATCCTGCCAGGCTCTGGGTCAGGACATG

FIG.15

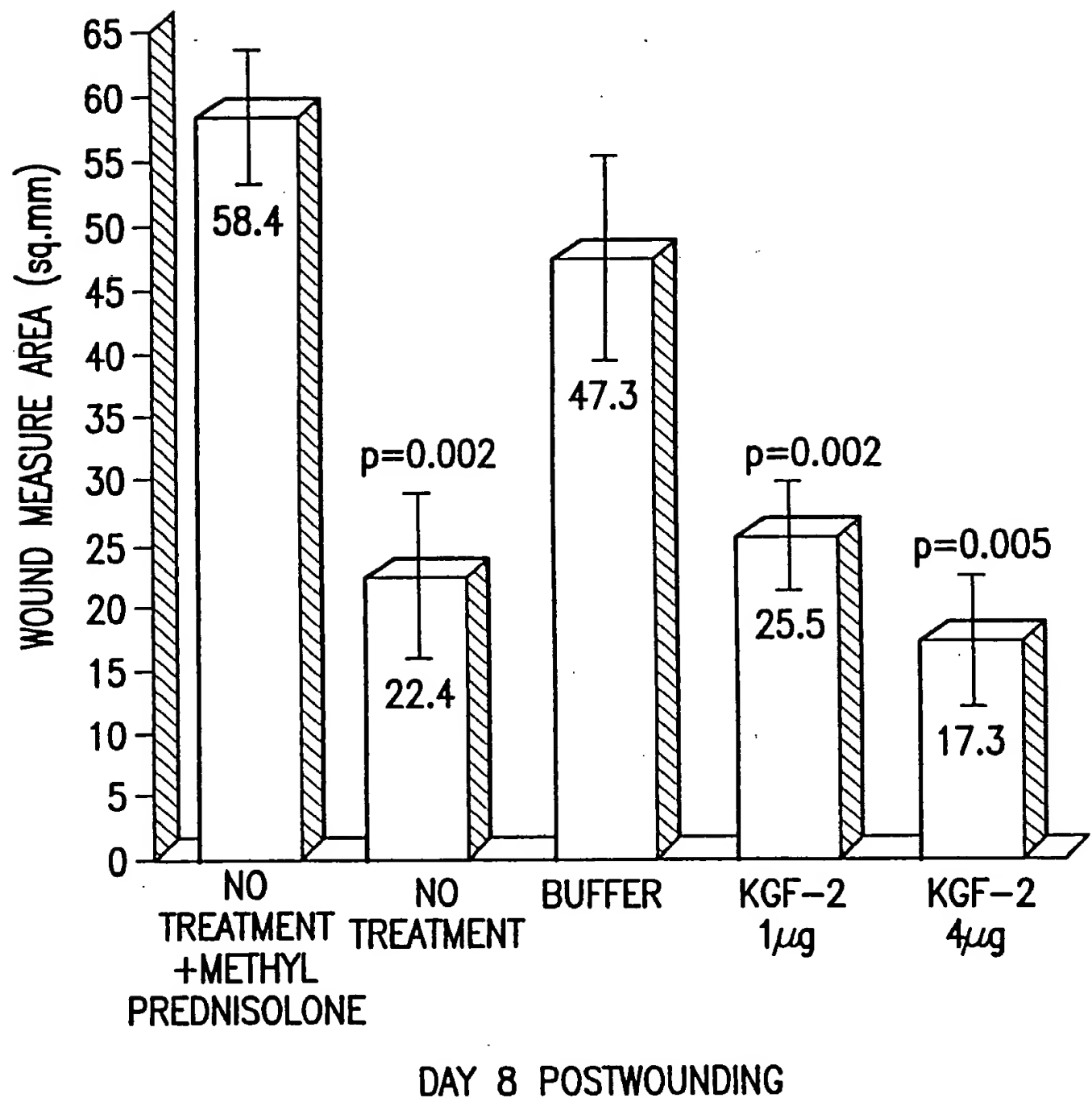
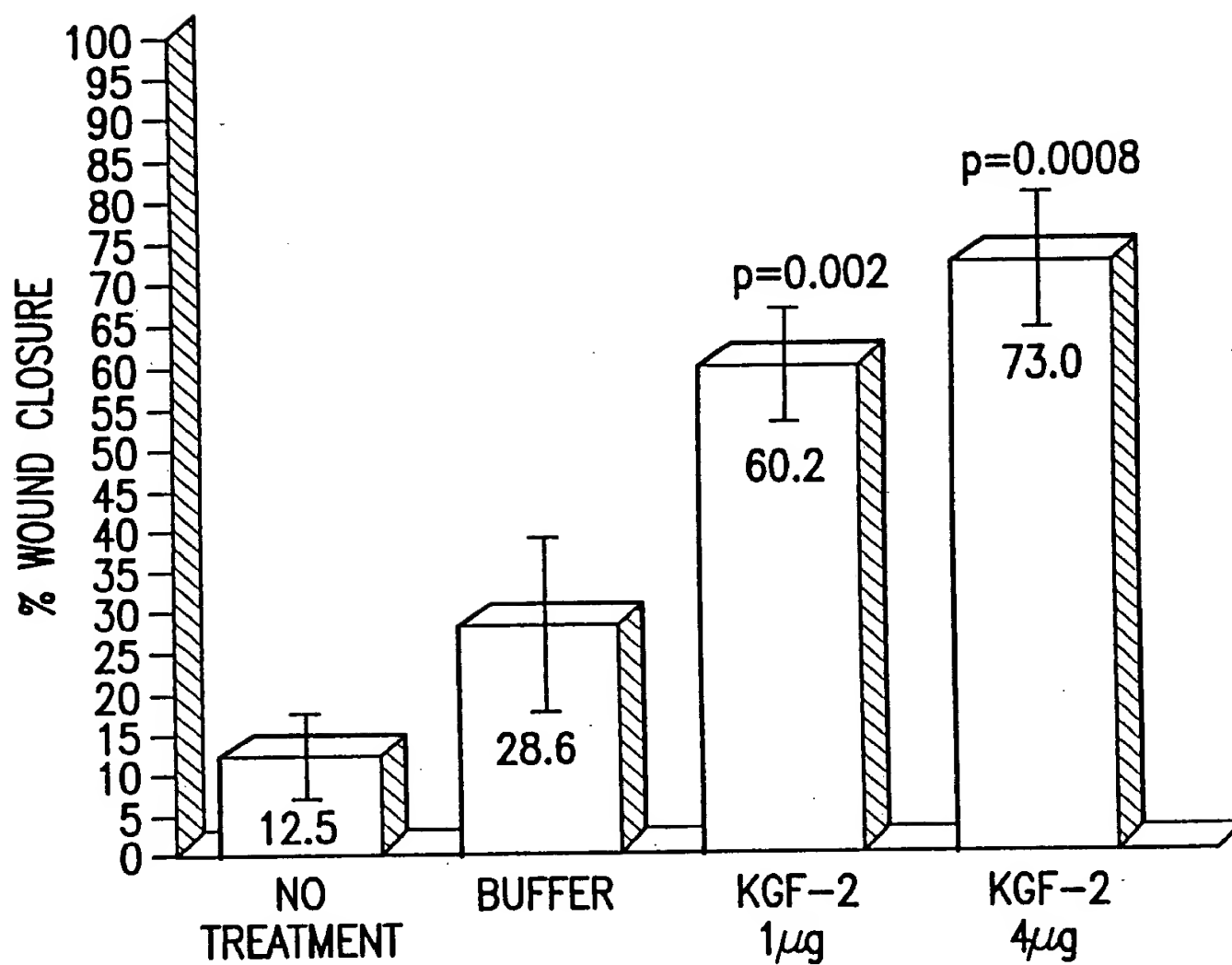


FIG.16



GLUCOCORTICOID TREATED ANIMALS

FIG.17

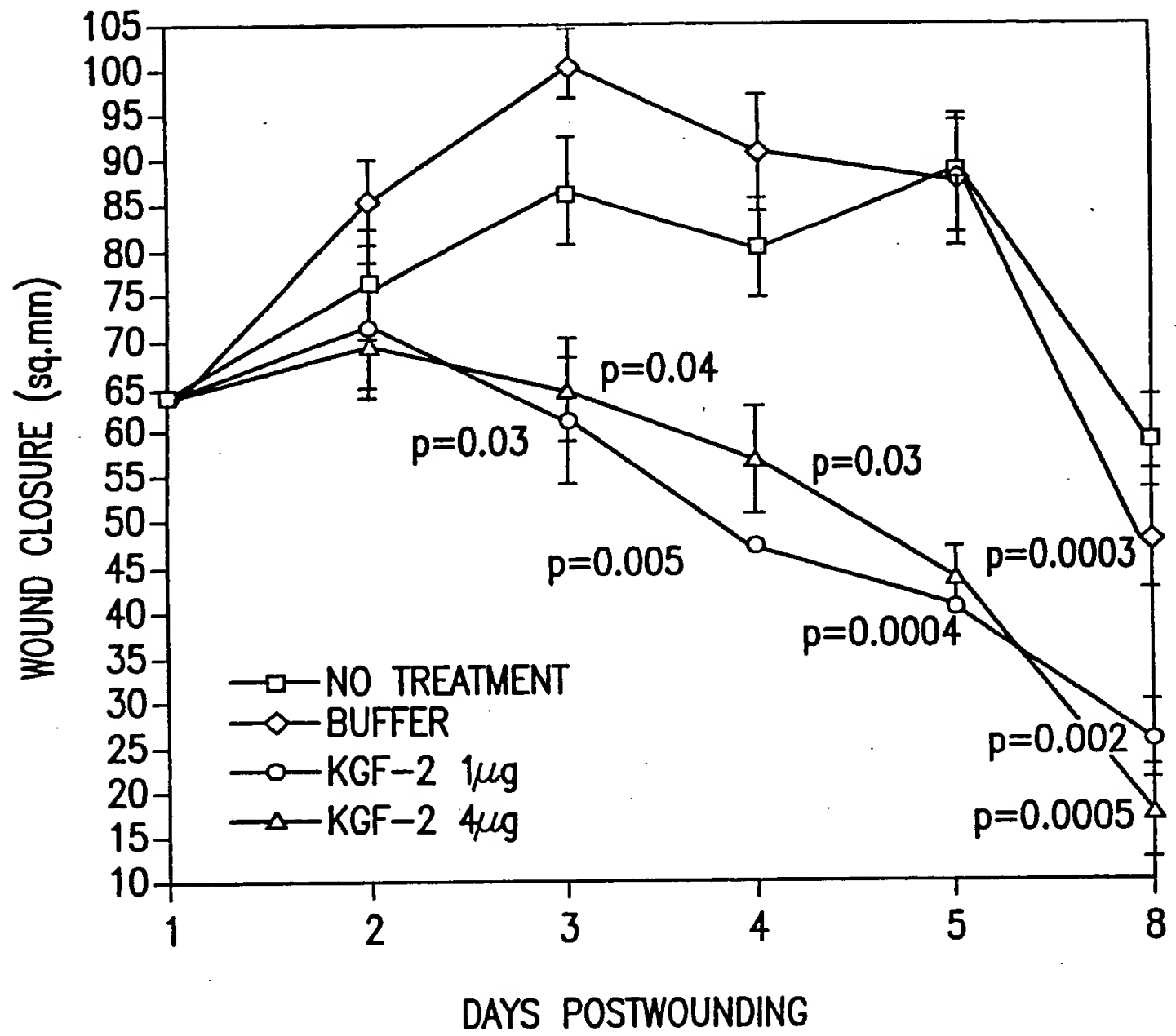


FIG.18

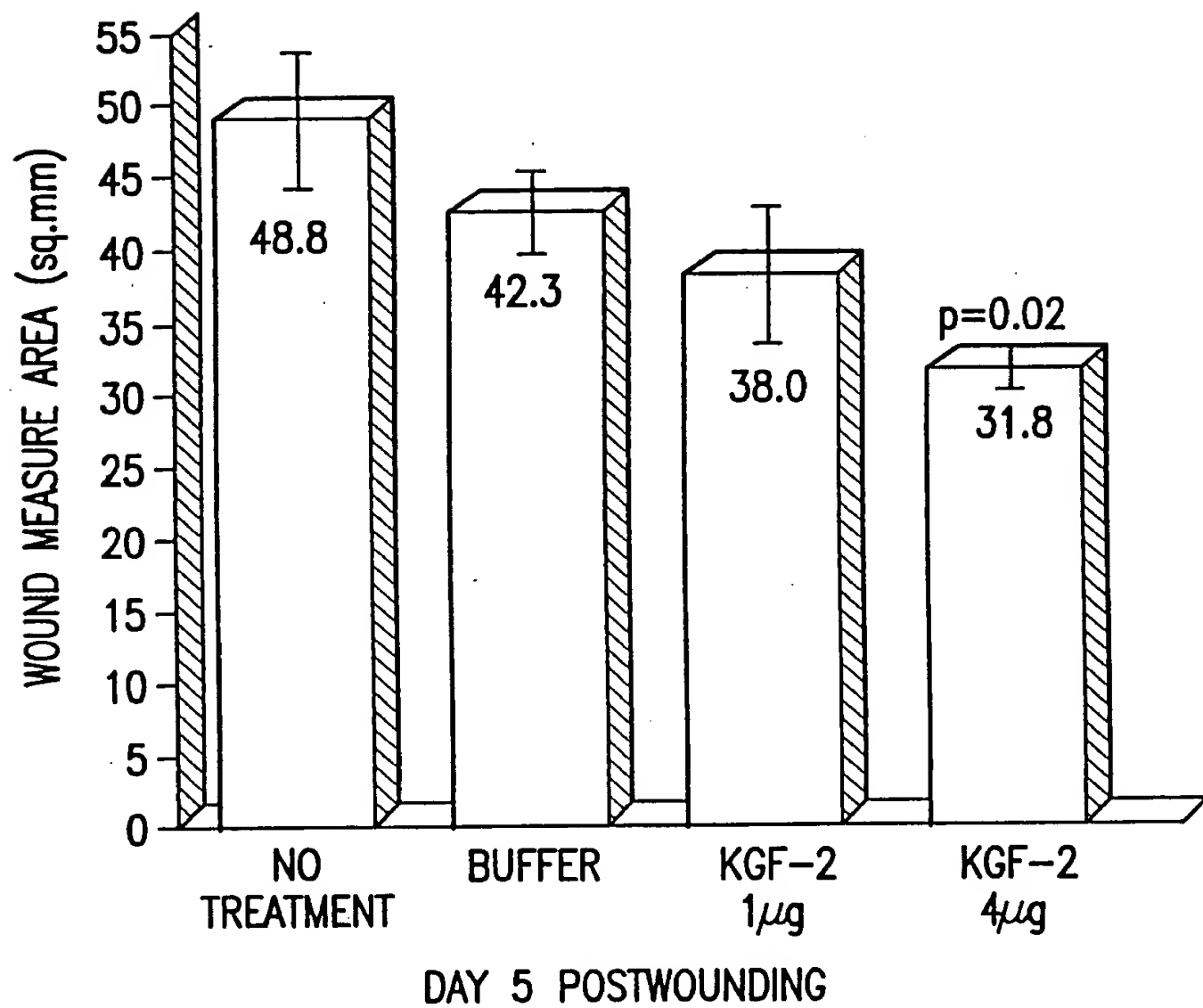
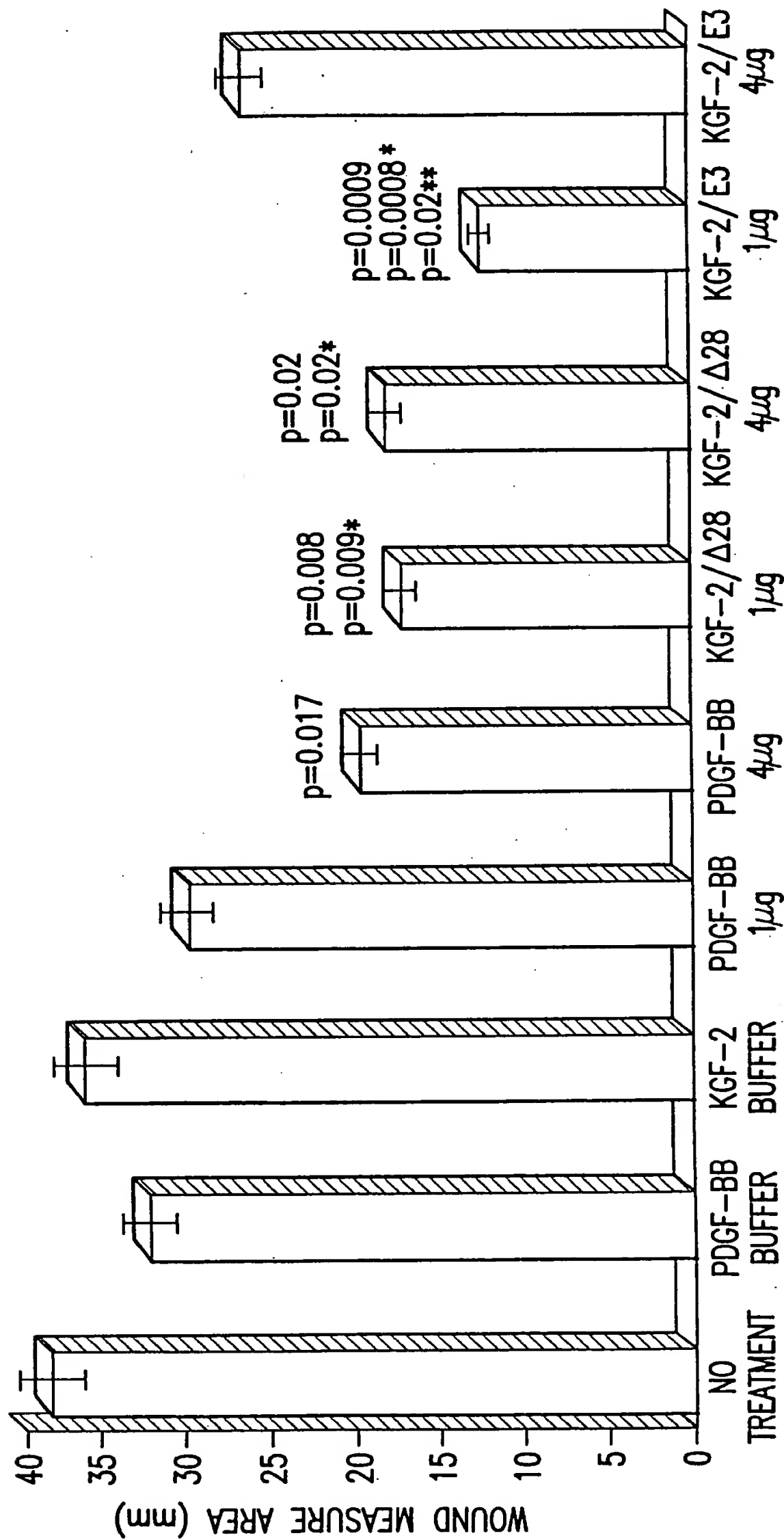


FIG.19A



DAY 10 POSTWOUNDING

FIG.19B

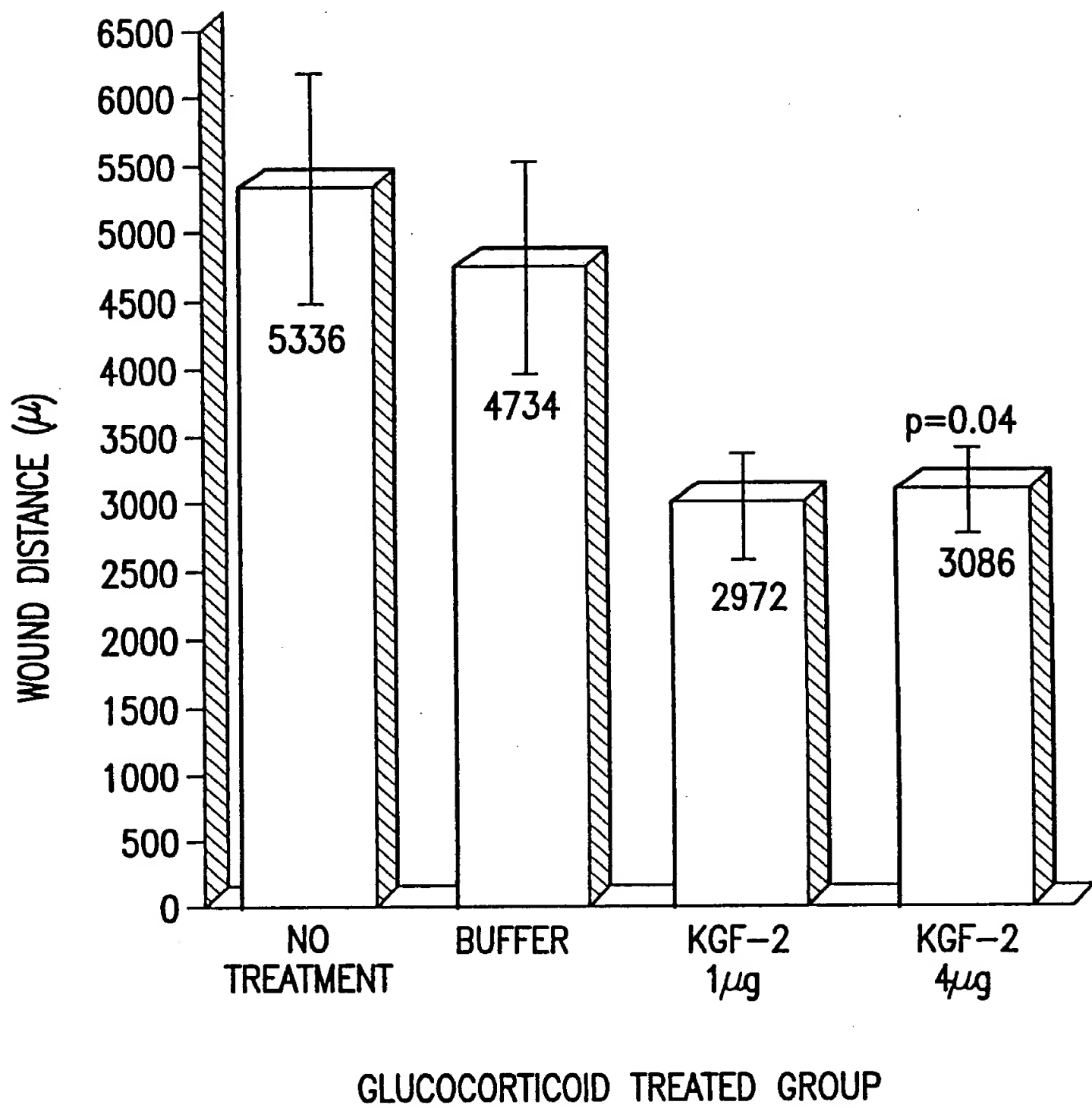


FIG.20

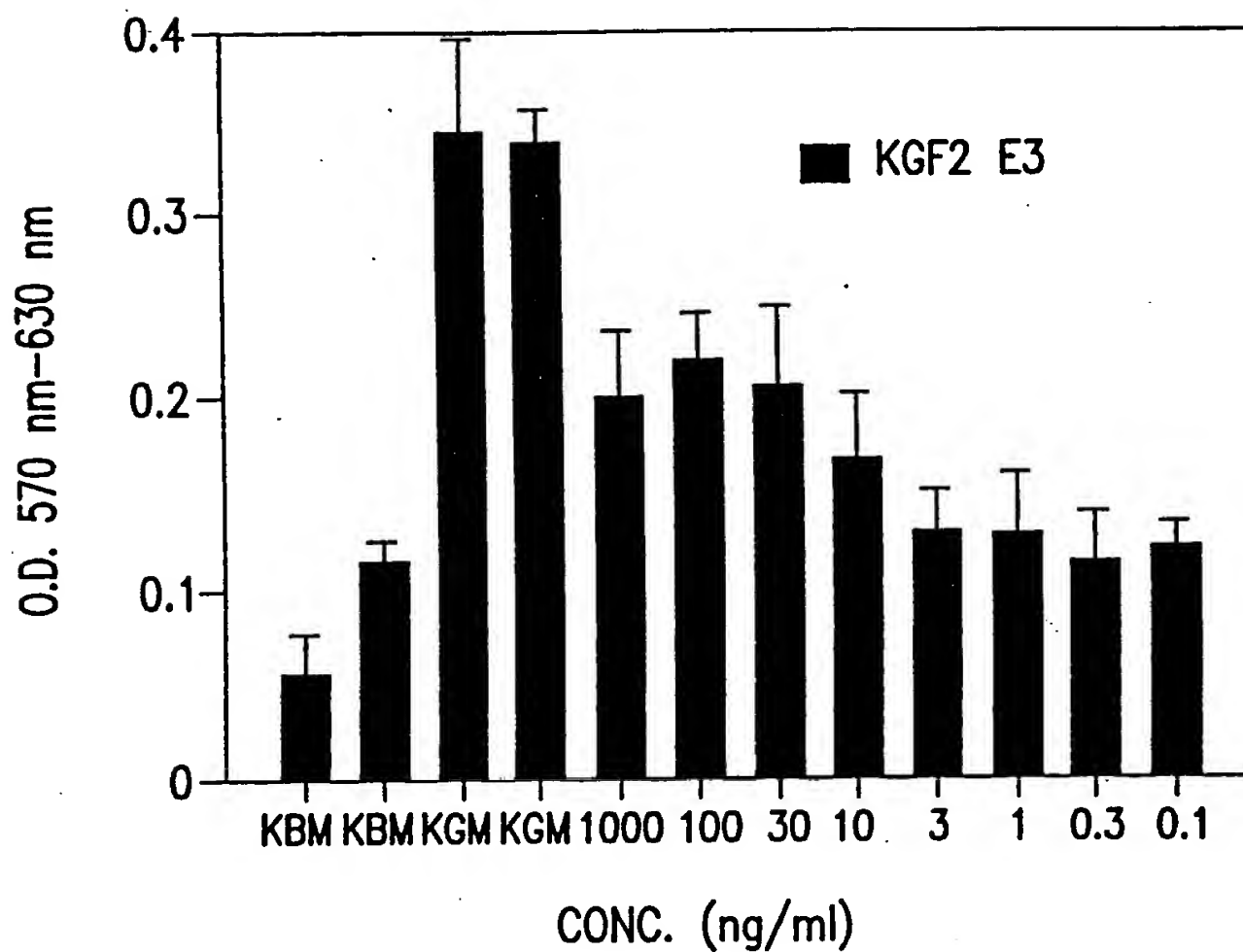


FIG.21A

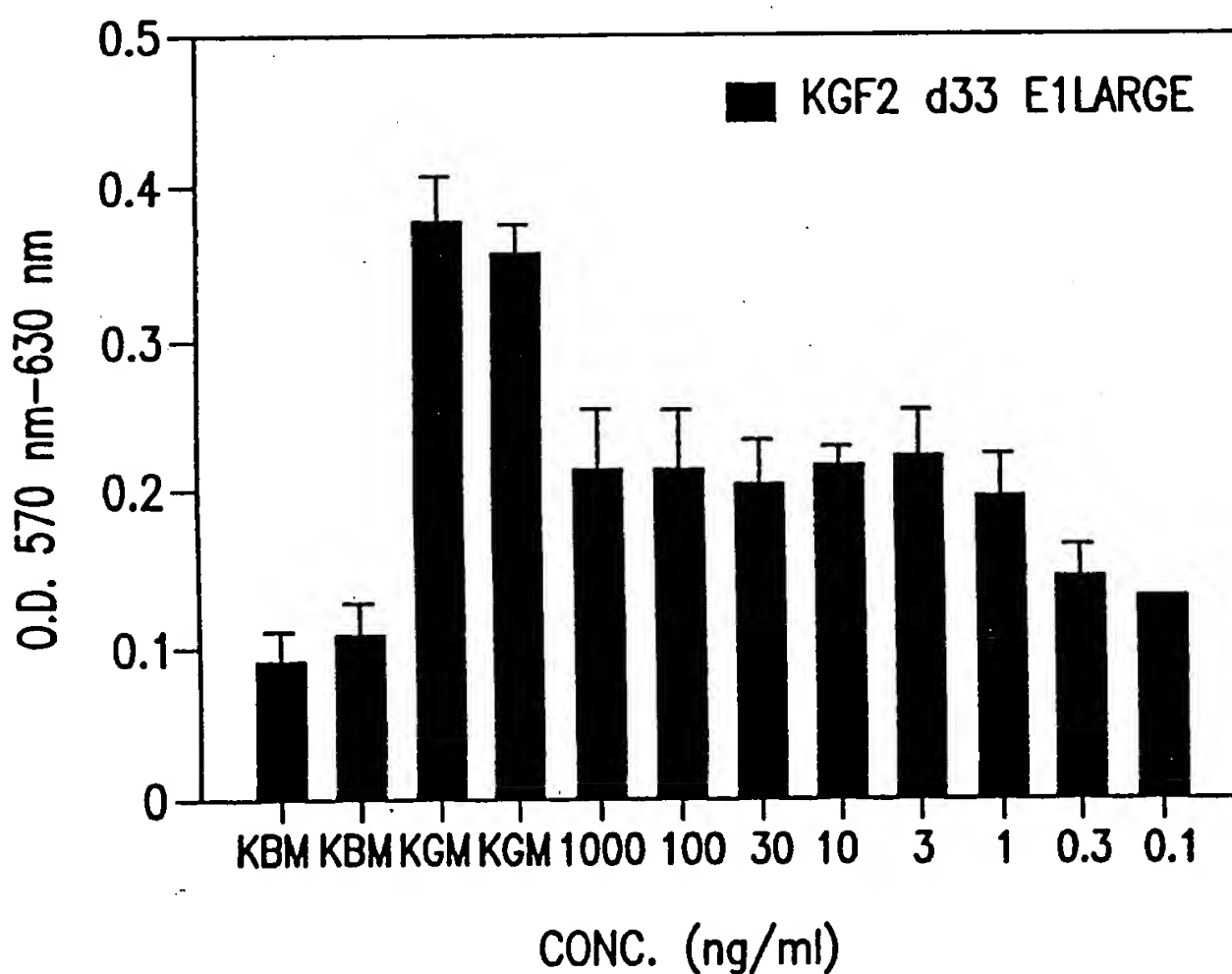
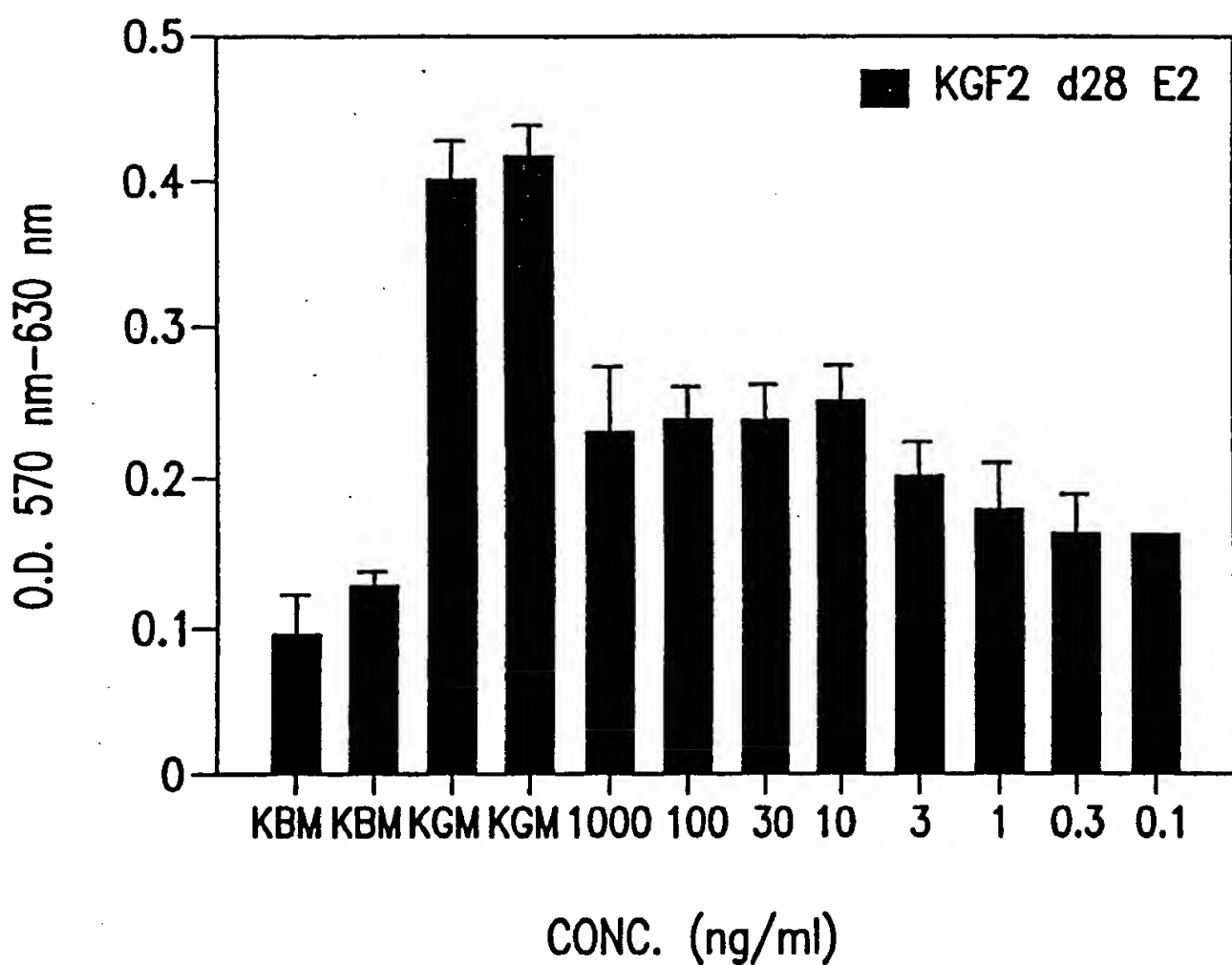


FIG.21B

BEST AVAILABLE COPY



BEST AVAILABLE COPY

FIG.21C

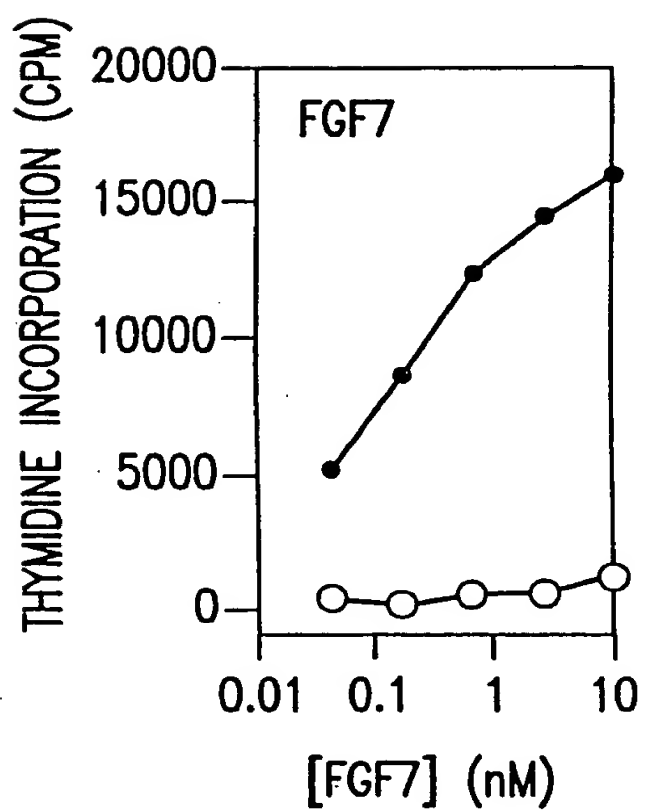


FIG.22A

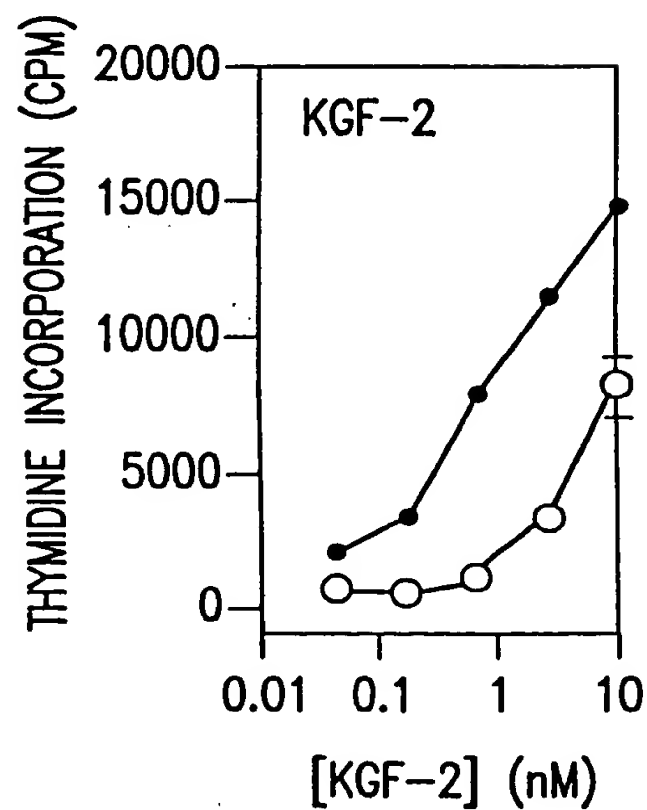


FIG.22A-1

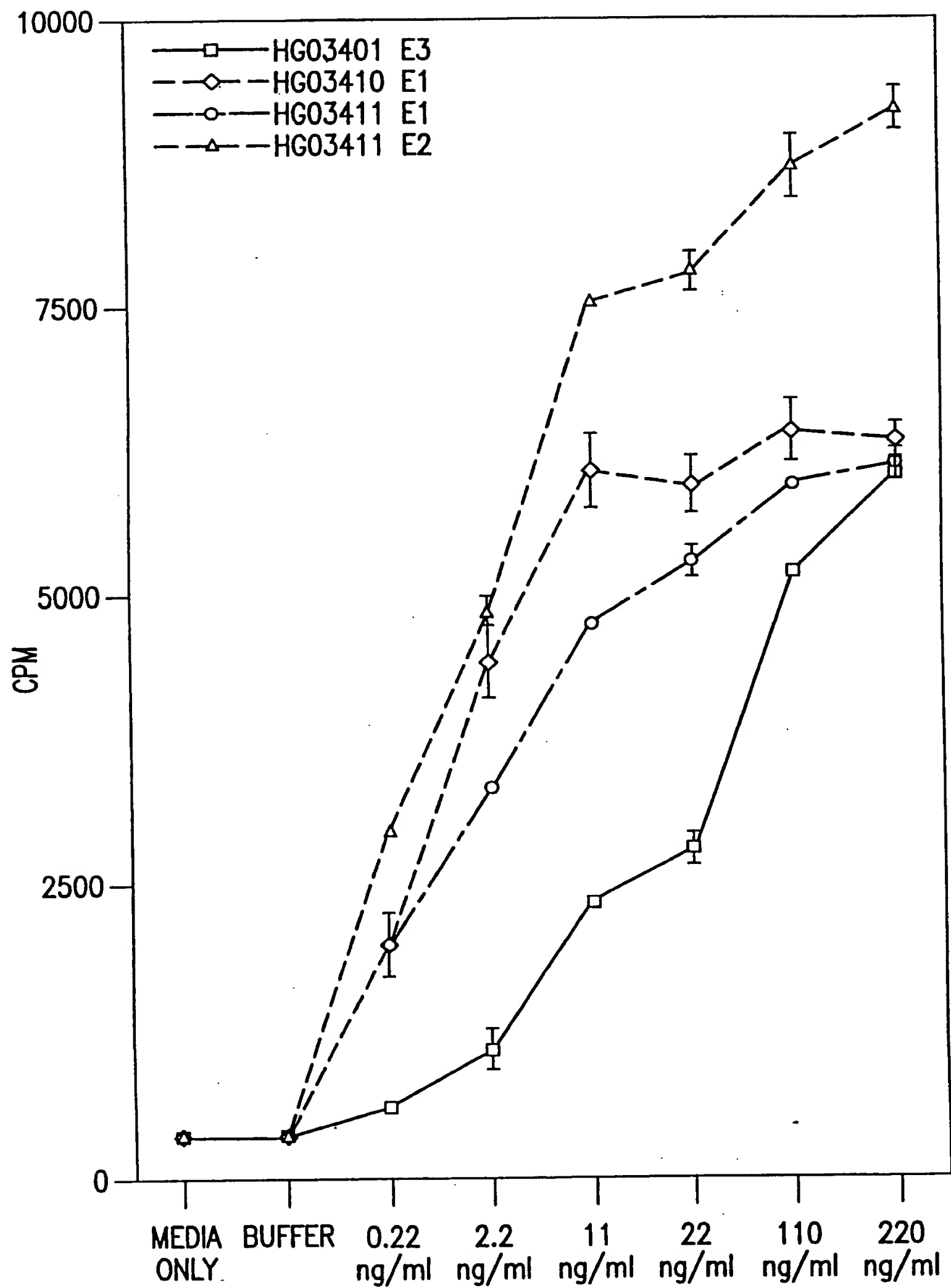


FIG.22B

BEST AVAILABLE COPY

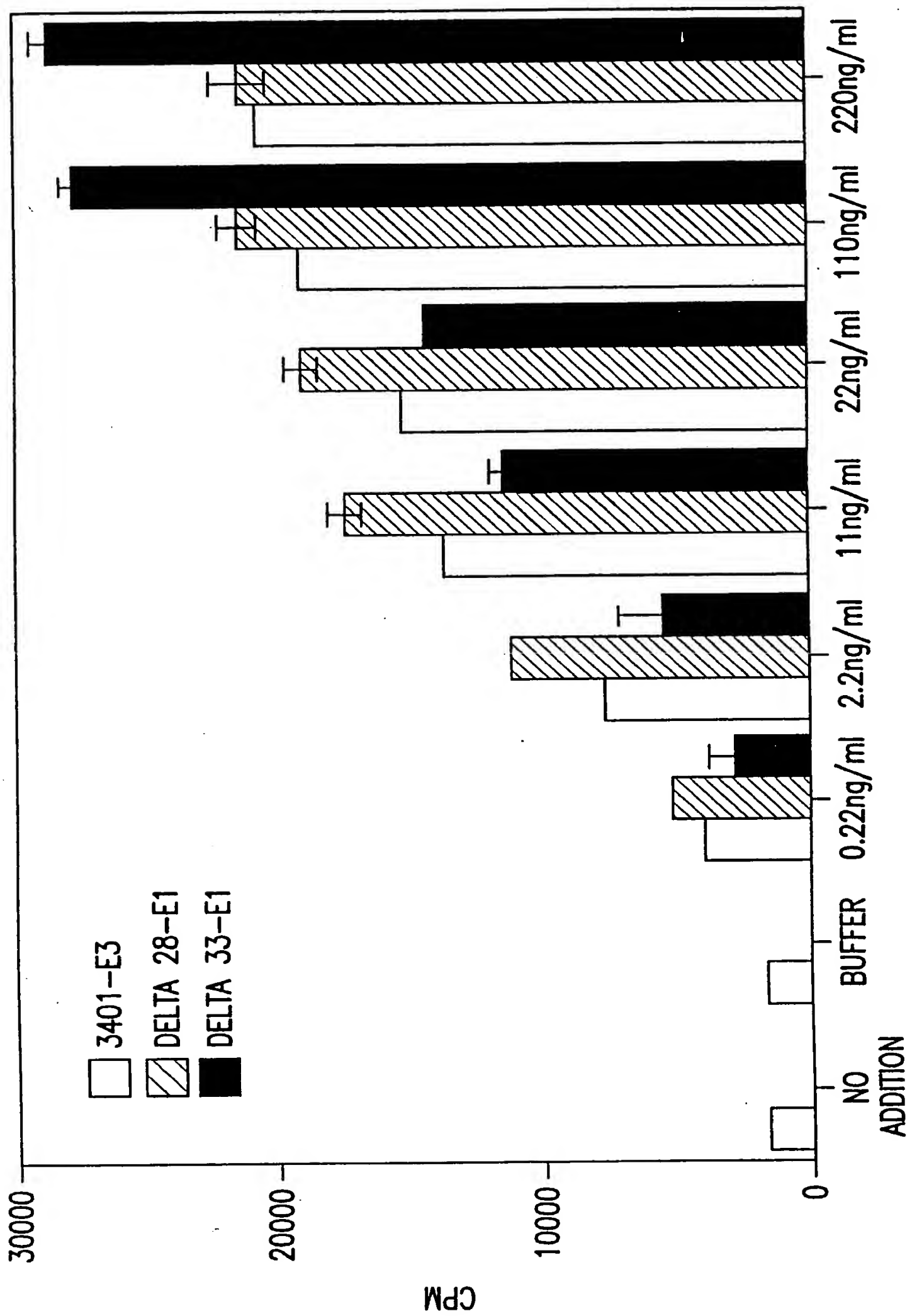


FIG.22C

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCT 60
MetThrCysGlnAlaLeuGlyGlnAspMetValSerProGluAlaThrAsnSerSerSer

TCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCTTACAACCACCTGCAG 120
SerSerPheSerSerProSerSerAlaGlyArgHisValArgSerTyrAsnHisLeuGln

GGTGACGTTCTGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA 180
GlyAspValArgTrpArgLysLeuPheSerPheThrLysTyrPheLeuLysIleGluLys

AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACA 240
AsnGlyLysValSerGlyThrLysLysGluAsnCysProTyrSerIleLeuGluIleThr

TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATG 300
SerValGluIleGlyValValAlaValLysAlaIleAsnSerAsnTyrTyrLeuAlaMet

AACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAG 360
AsnLysLysGlyLysLeuTyrGlySerLysGluPheAsnAsnAspCysLysLeuLysGlu

AGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420
ArgIleGluGluAsnGlyTyrAsnThrTyrAlaSerPheAsnTrpGlnHisAsnGlyArg

CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG 480
GlnMetTyrValAlaLeuAsnGlyLysGlyAlaProArgArgGlyGlnLysThrArgArg

AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG 525
LysAsnThrSerAlaHisPheLeuProMetValValHisSer *

FIG.24A

ATGACTTGCCAGGCACTGGGTCAAGACATGGTTTCCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 70
TACTGAACGGTCOGTGACCCAGTTCTGTACCAAAGGGCCCTTCGATGGTTGTCGAGGTCGAGATCGAAGT
M T C Q A L G Q D M V S P E A T N S S S S S F
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GCAGCCCATCTAGCGCAGGTCGTCAAGTTCGCTCTTACAACCACTTACAGGGTGATGTTGTTGGCGCAA
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 140
CGTCGGGTAGATCGCGTCCAGCAGTGCAAGCGAGAATGTTGGTGAATGTCCCACTACAAGCAACCGCGTT
S S P S S A G R H V R S Y N H L Q G D V R W R K
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
ACTGTTGAGCTTTACCAAGTACTTCCTGAAAATCGAAAAAAGCGTAAAGTTTCTGGGACCAAGAAGGAG
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 210
TGACAAGTCGAAATGGTTCATGAAGGACTTTTAGCTTTTTTGGCATTTCAAAGACCCTGGTTCTTCCTC
L F S F T K Y F L K I E K N G K V S G T K K E
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
AACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACA
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 280
TTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTAGCCTCAACAACGGCAGTTTCGTAATTGT
N C P Y S I L E I T S V E I G V V A V K A I N
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GCAACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAA
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 350
CGTTGATAATGAATCGGTACTTGTCTTCCCCTTTGAGATACCGAGTTTCTTAAATTGTTACTGACATT
S N Y Y L A M N K K G K L Y G S K E F N N D C K
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 420
CGACTTCCTCTCCTATCTCCTTTTACCTATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCC
L K E R I E E N G Y N T Y A S F N W Q H N G R
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
CAAATGTATGTGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACAGGAAGGAAAAACACCT
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 490
GTTTACATACACCGTAACTTACCTTTTCTCGAGGTTCTCTCTGTCTTTTGTGCTTCCTTTTGTGGA
Q M Y V A L N G K G A P R R G Q K T R R K N T
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
CTGCTCACTTTCTTCCAATGGTGGTACACTCATAG
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 525
GACGAGTGAAAGAAGGTTACCACCATGTGAGTATC
S A H F L P M V V H S
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

FIG.24B

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCTTACAACCAC
CTGCAGGGTGACGTTCTGTTGGCGTAACTGTTCTTTTACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIE
KNGKVSGETKKENCPYSILEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKL
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.25

ATGGCTGGTCGTCACGTTCTTACAACCACCTGCAGGGTGACGTTCTTGGCGT
AACTGTTCTTTTACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG
GGGAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATA
GAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAA
ATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG
AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIEKNGKVSGETKKENCPYSILEITSVEIGV
VAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.26

ATGGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATA
ACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTA
GCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAGAATTAAACAATGACTGTAAG
CTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAG
CATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGA
CAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCA
TAG

MVRWRKLFSTKYFLKIEKNGKVS GTKKENCPYSILEITSVEIGVVAVKAINS NYYLAM
NKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTR
RKNTSAHFLPMVVHS.

FIG.27

ATGGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCAT
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCA
ACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAGAATTAAAC
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATC
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCA
ATGGTGGTACACTCATAG

MEKNGKVS GTKKENCPYSILEITSVEIGVVAVKAINS NYYLAMNKKGKLYGSKEFNND
CKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH
S.

FIG.28

ATGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGT
TGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAAC
TCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA
AATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTA
TGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA
ACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MENCPYSILEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGY
NTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.29

ATGGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACT
CTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAA
ATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAA
CACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.30

ATGGGGAAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAG
GATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGA
GGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACA
CGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT
RRKNTSAHFLPMVVHS.

FIG.31

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCTTACAACCAC
CTGCAGGGTGACGTTCTGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT
GACTGTAAGCTGAAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSTKYFLKIE
KNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKL
K

FIG.32

ATGGCTGGTCGTCACGTTCTTACAACCACCTGCAGGGTGACGTTCTGTTGGCGT
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG
GGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAG

MAGRHVRSYNHLQGDVRWRKLFSTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGV
VAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLK

FIG.33

C-37 To Ser

ATGACCTCTCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTGTTCTTACAACCAC
CTGCAGGGTGACGTTGTTGGCGTAAACTGTTCTTTTACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

FIG.34

C-106 To Ser

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTGTTCTTACAACCAC
CTGCAGGGTGACGTTGTTGGCGTAAACTGTTCTTTTACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

FIG.35

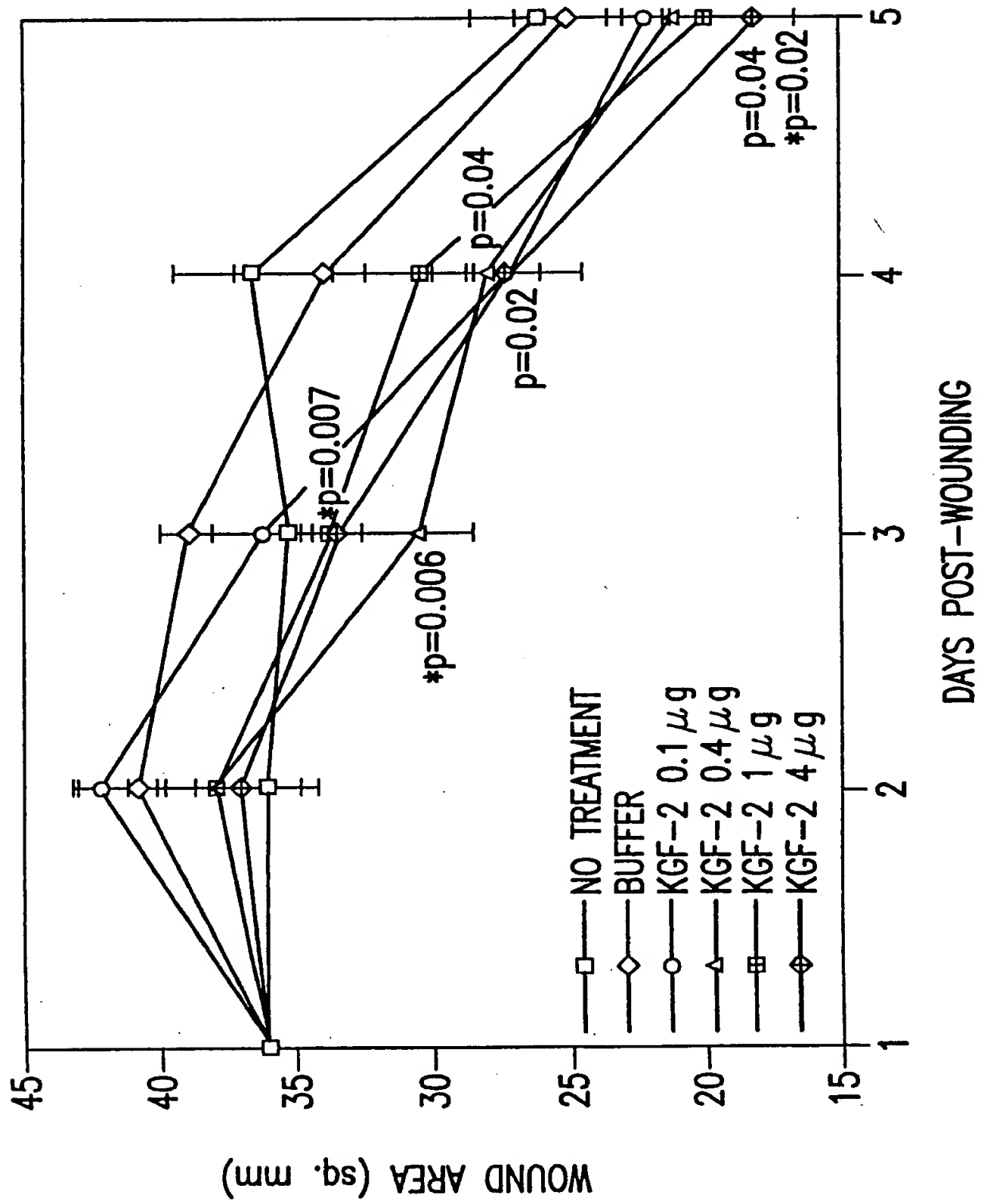


FIG. 36

EFFECT OF KGF-2 Δ33 ON NORMAL WOUND HEALING RAT MODEL

TREATMENT GROUPS	WOUND SIZE (mm)	% WOUND CLOSURE	HISTOLOGICAL SCORE	RE-EPITH. (μm)	BrdU SCORE
NO TREATMENT	25.9±2.5	58.8±3.7	6.8±0.2	1142±141	3.8±0.4
BUFFER	25.1±1.7	60.2±2.6	6.4±0.2	923±61	5.0±0.4
KGF-2/Δ33 (0.1 μg)	22.0±0.9	65±1.4	6.8±0.2	1275±148	4.6±0.7
KGF-2/Δ33 (0.4 μg)	21.1±1.4	68.4±2.4	8.0±0.5 p=0.0445*	1310±182	4.2±0.7
KGF-2/Δ33 (1.0 μg)	19.9±1.5	66.2±2.1	8.4±0.4 p=0.0159* p=0.0053†	1389±115 p=0.0074†	3.3±0.25 p=0.0217†
KGF-2/Δ33 (4.0 μg)	18.1±1.6 p=0.0398* p=0.0200†	71.2±2.6 p=0.0367* p=0.0217†	8.5±0.3 p=0.0047* p=0.0445†	1220±89 p=0.0254†	5.3±0.9

FIG. 37

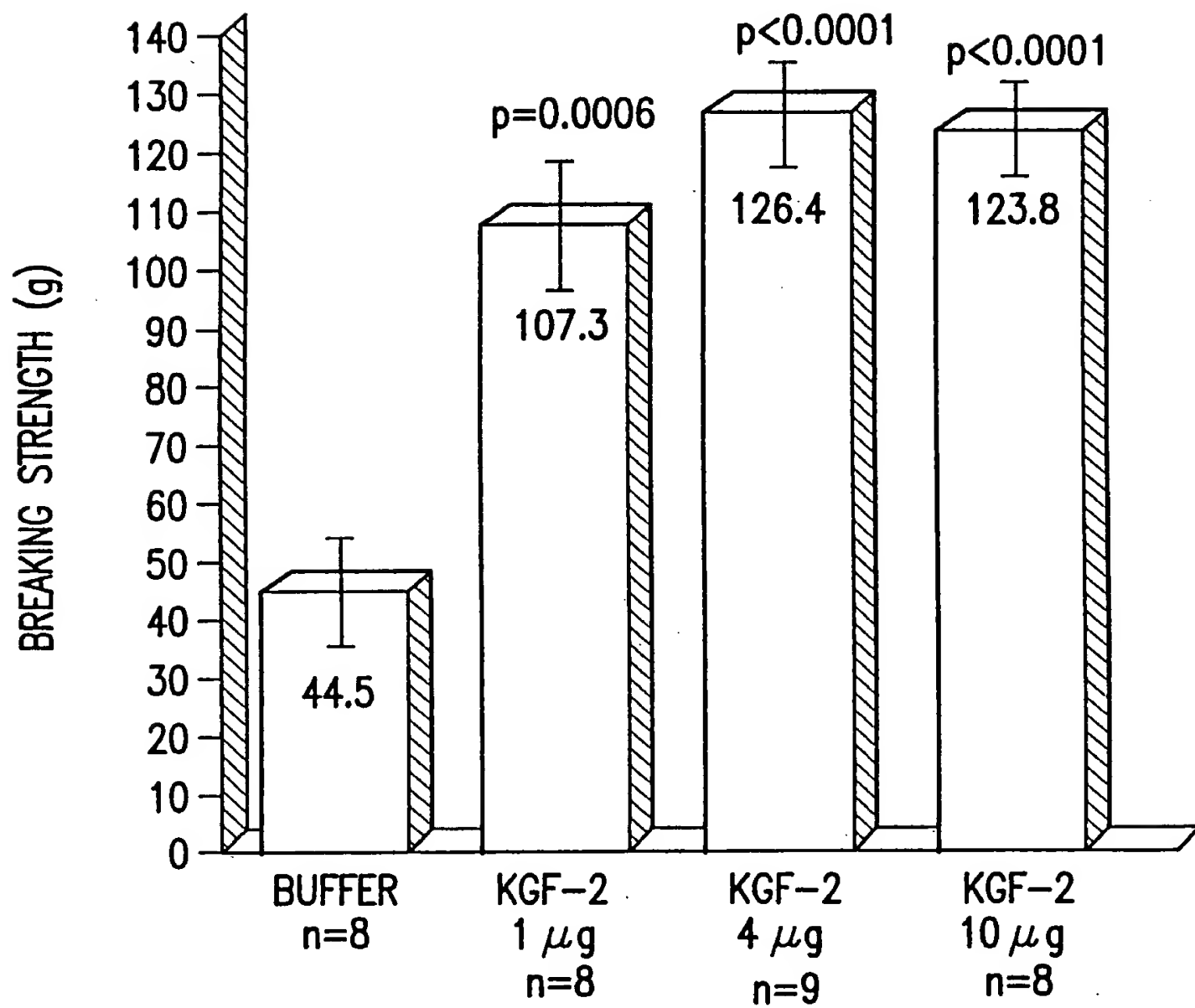


FIG.38

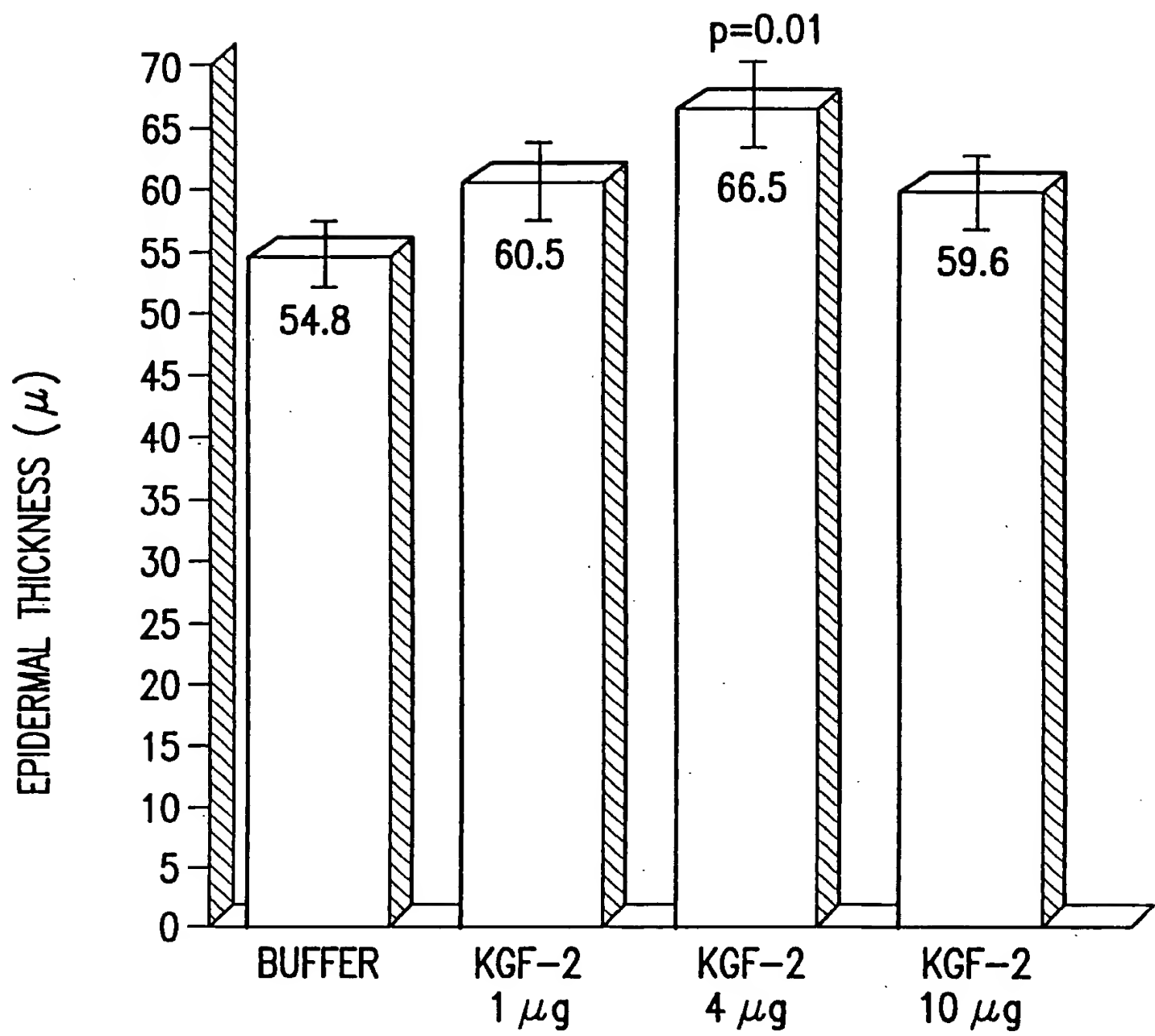


FIG.39

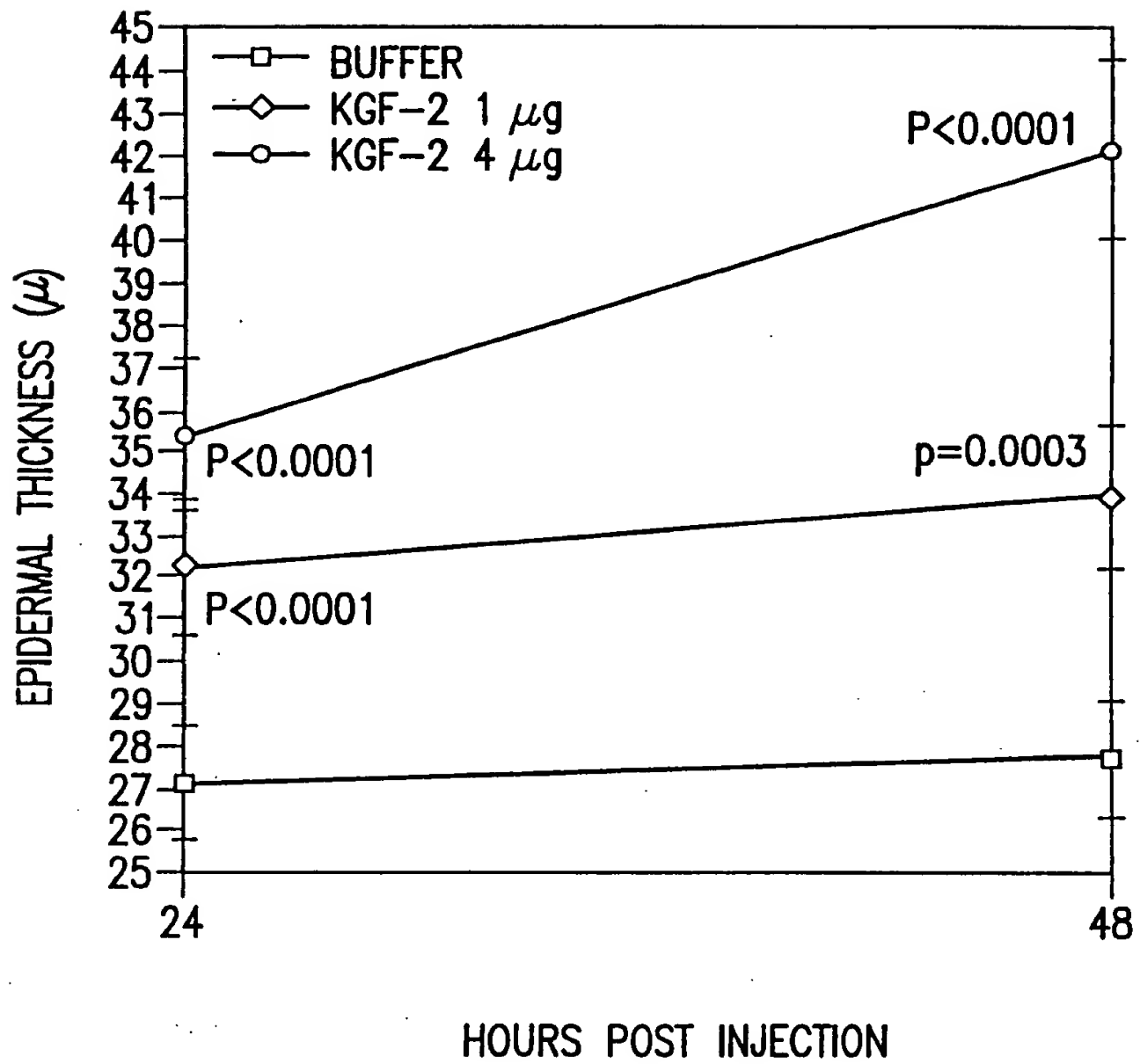


FIG.40

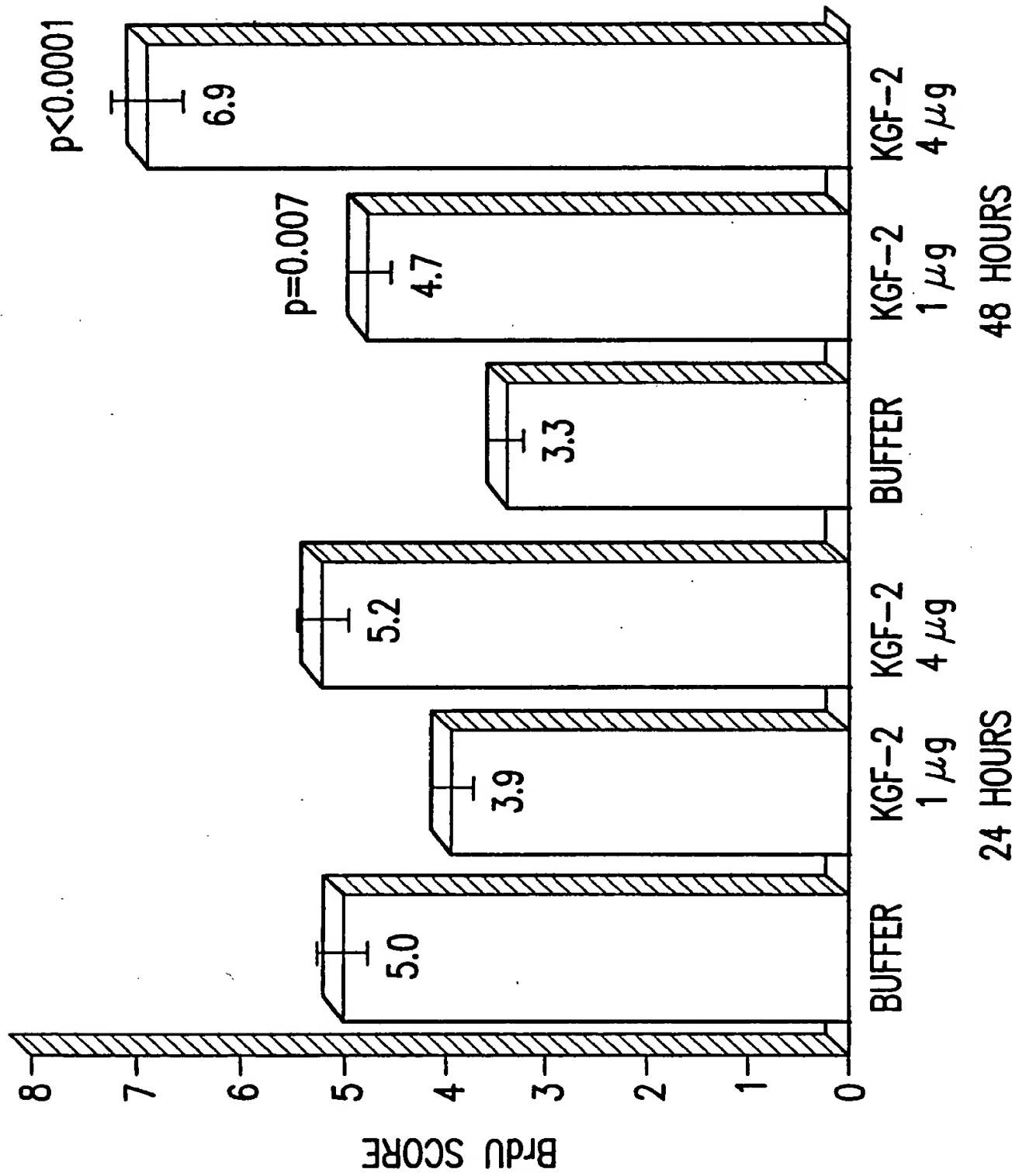


FIG.41

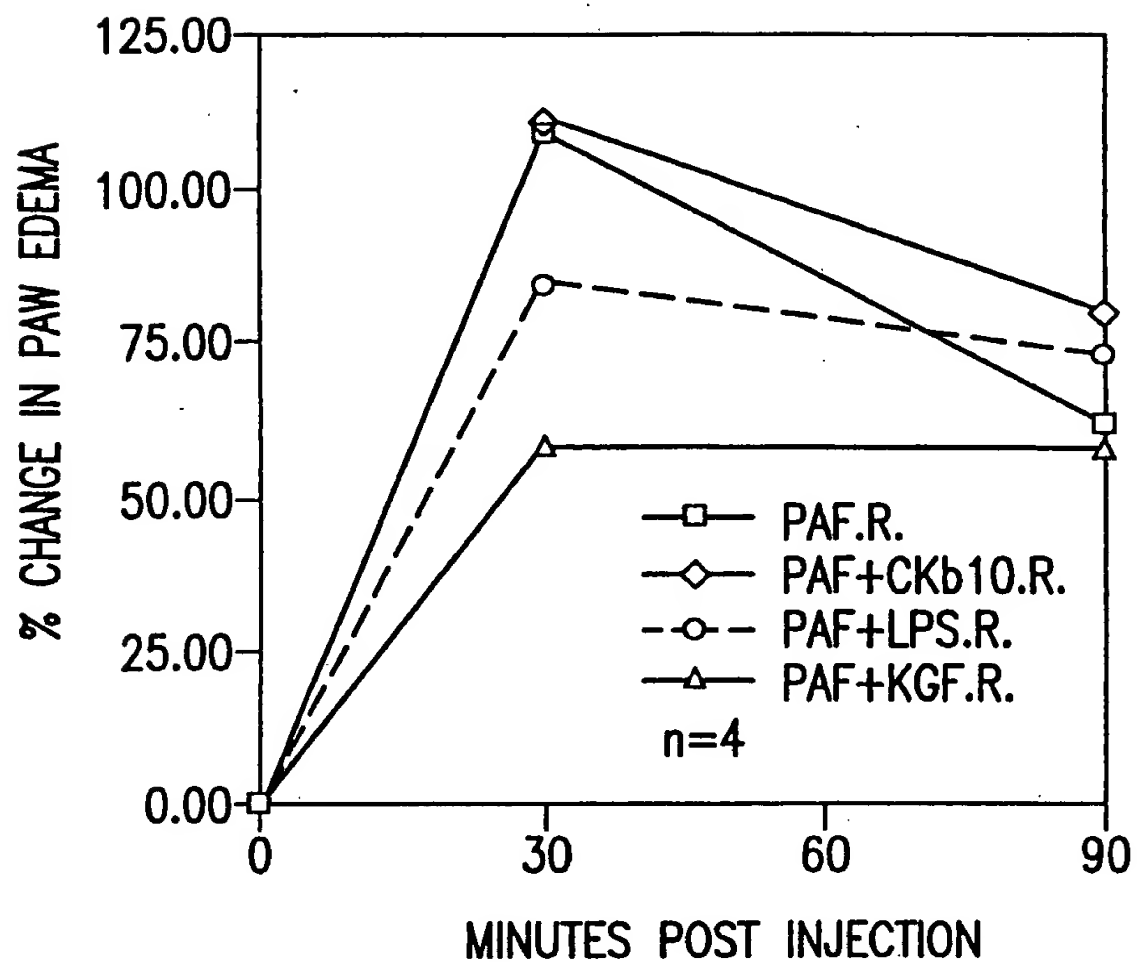


FIG.42A

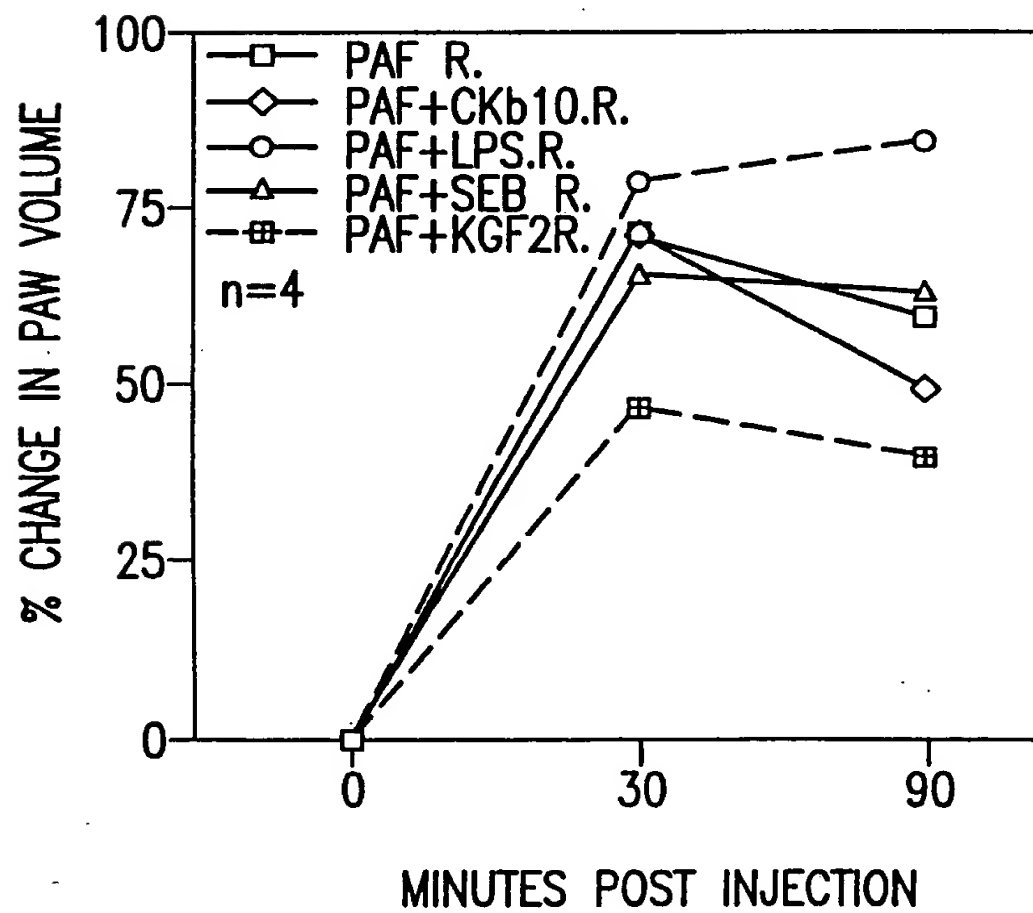


FIG.42B

EFFECT OF KGF-2 $\Delta 33$ ON PAF-INDUCED PAW EDEMA IN LEWIS RATS

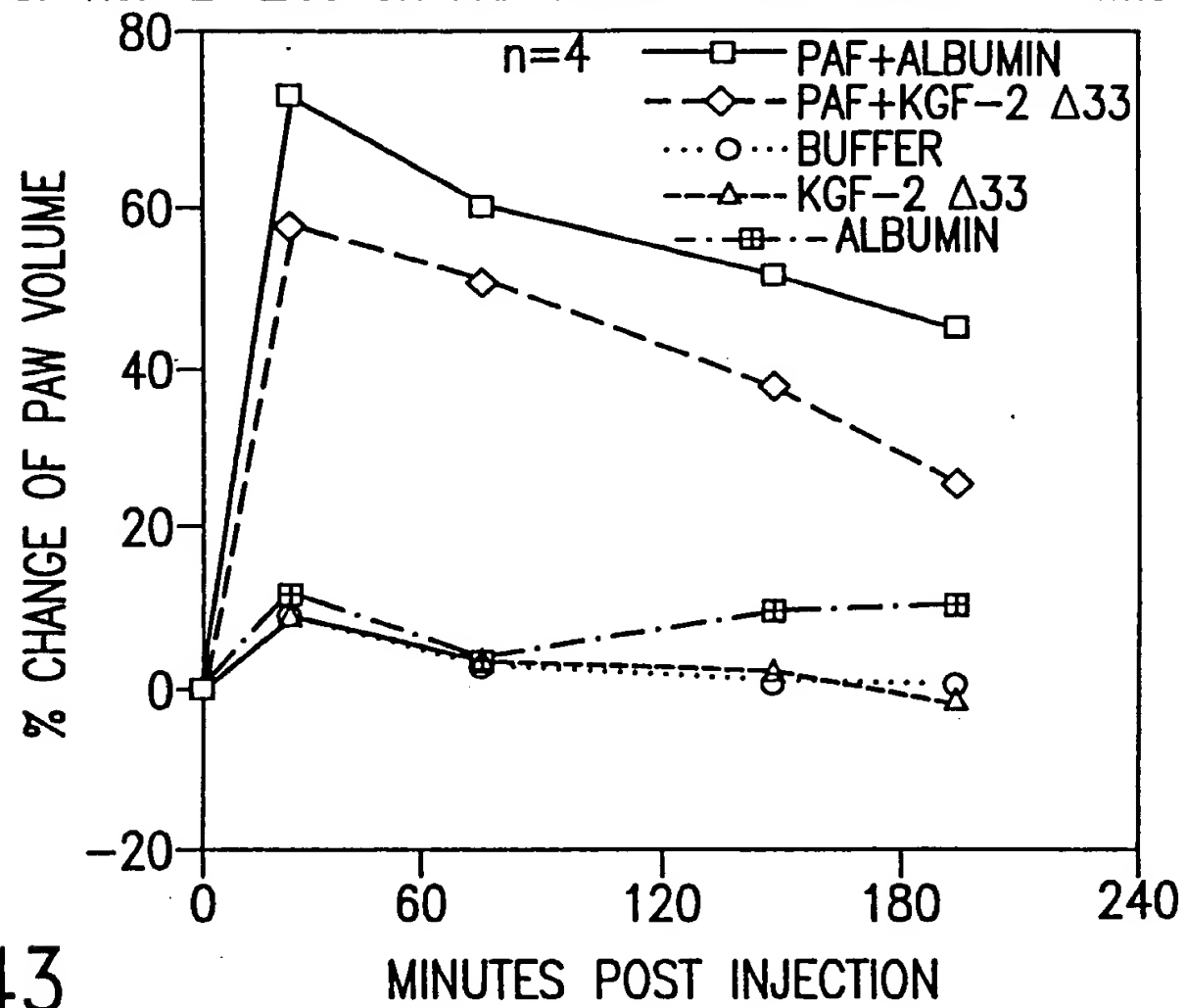


FIG.43

EFFECT OF KGF-2 $\Delta 33$ ON SURVIVAL OF WHOLE BODY IRRADIATED Balb/c MICE

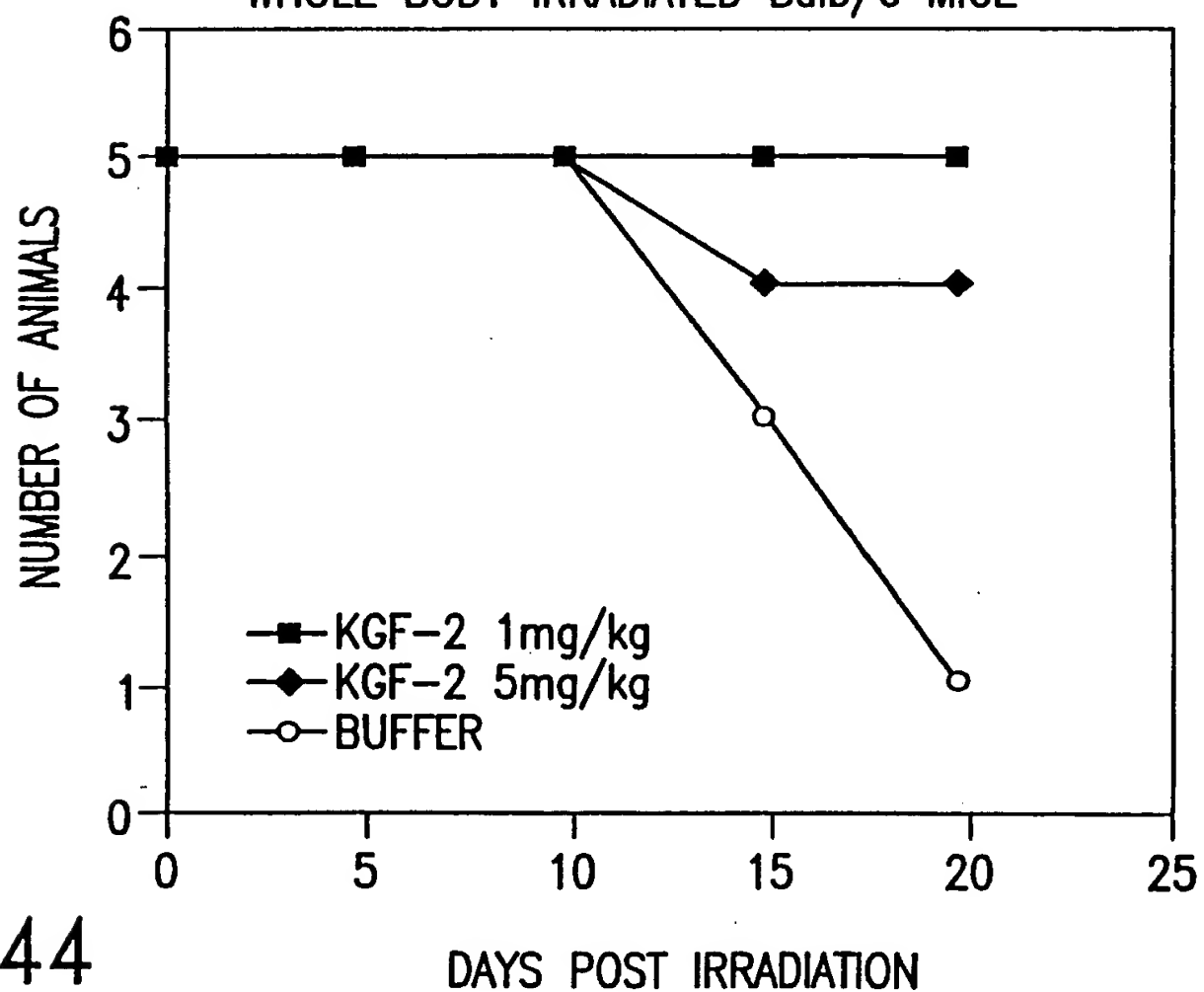


FIG.44

EFFECT OF KGF-2 Δ 33 ON BODY WEIGHT OF IRRADIATED MICE

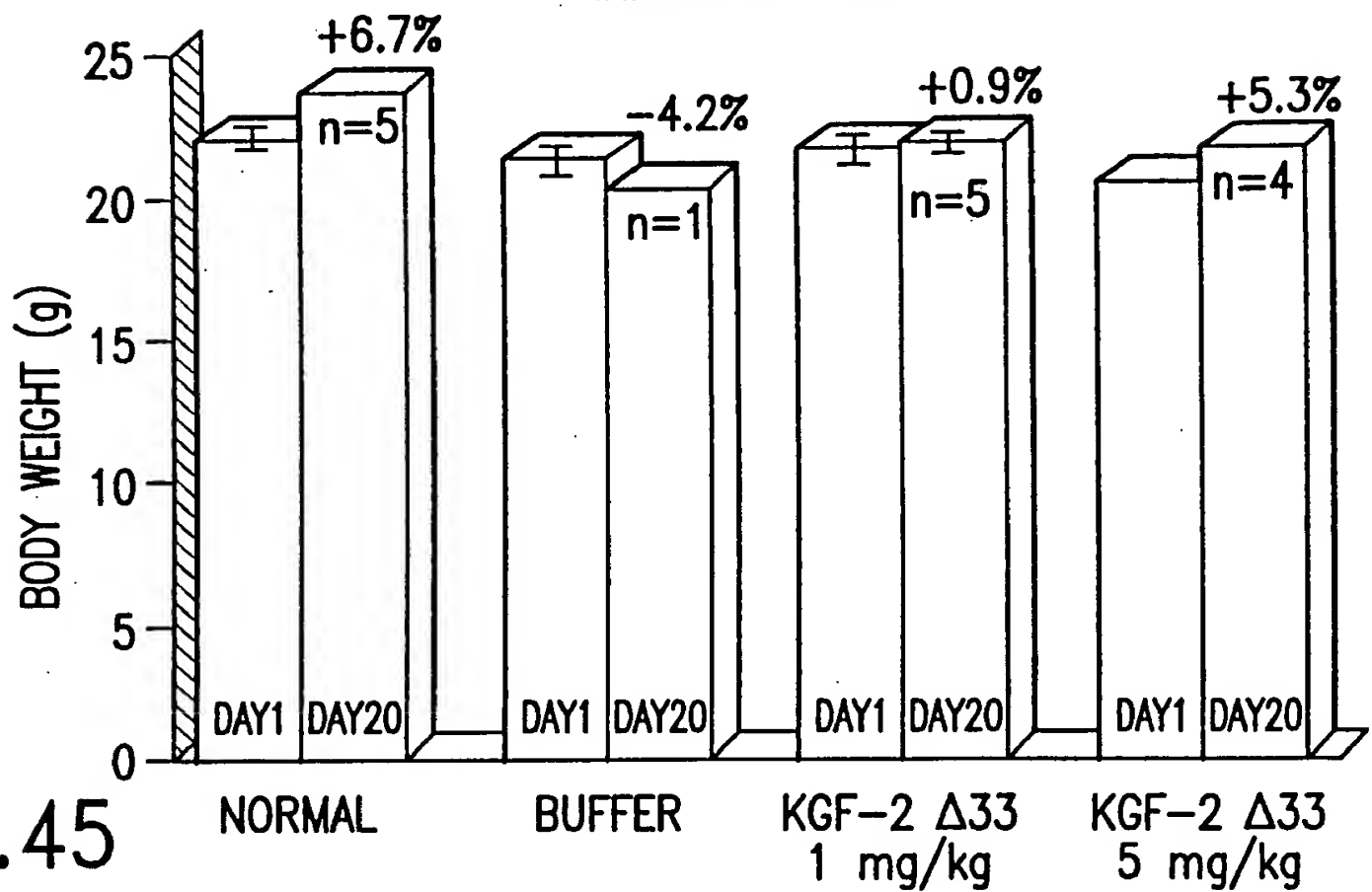


FIG.45

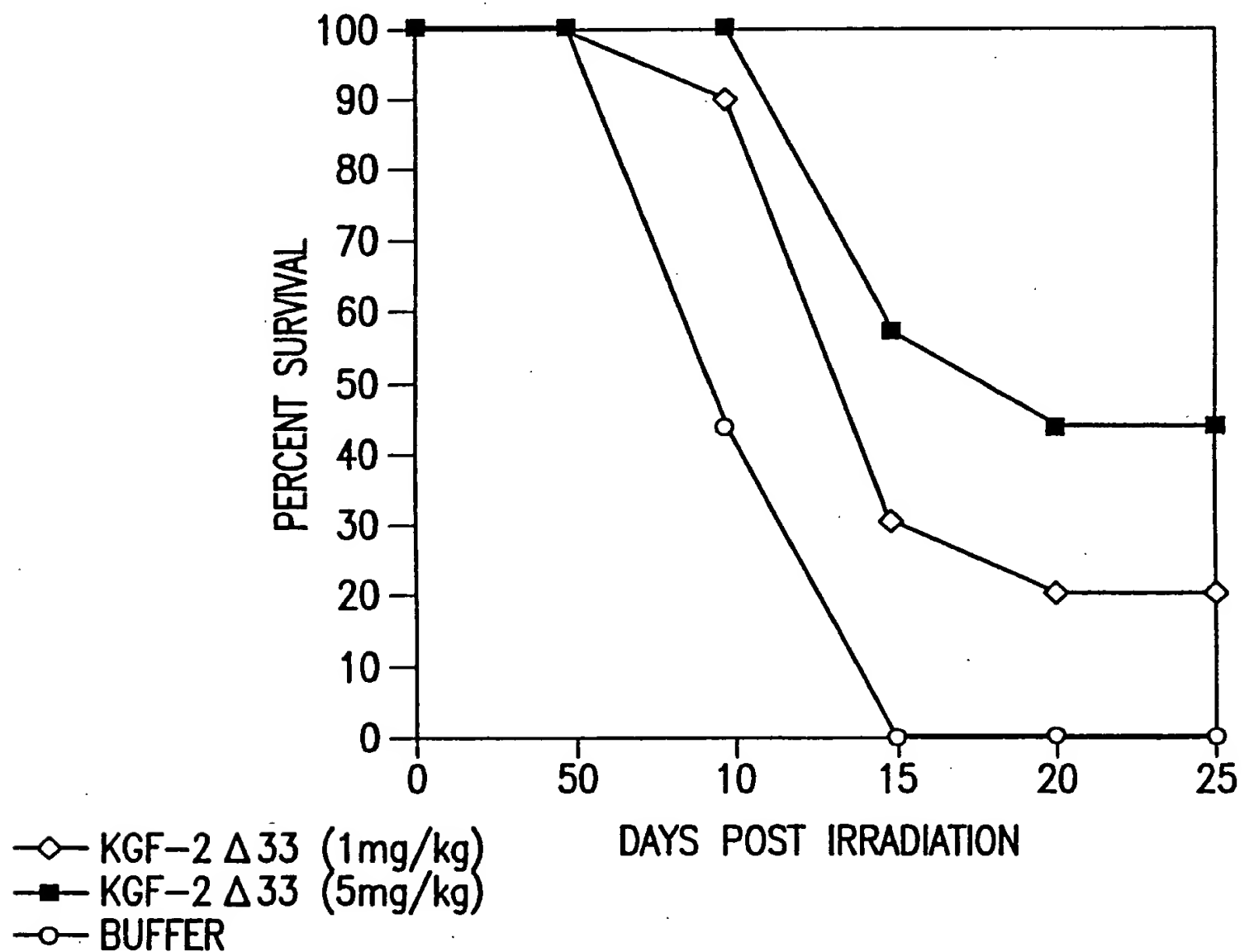


FIG.46

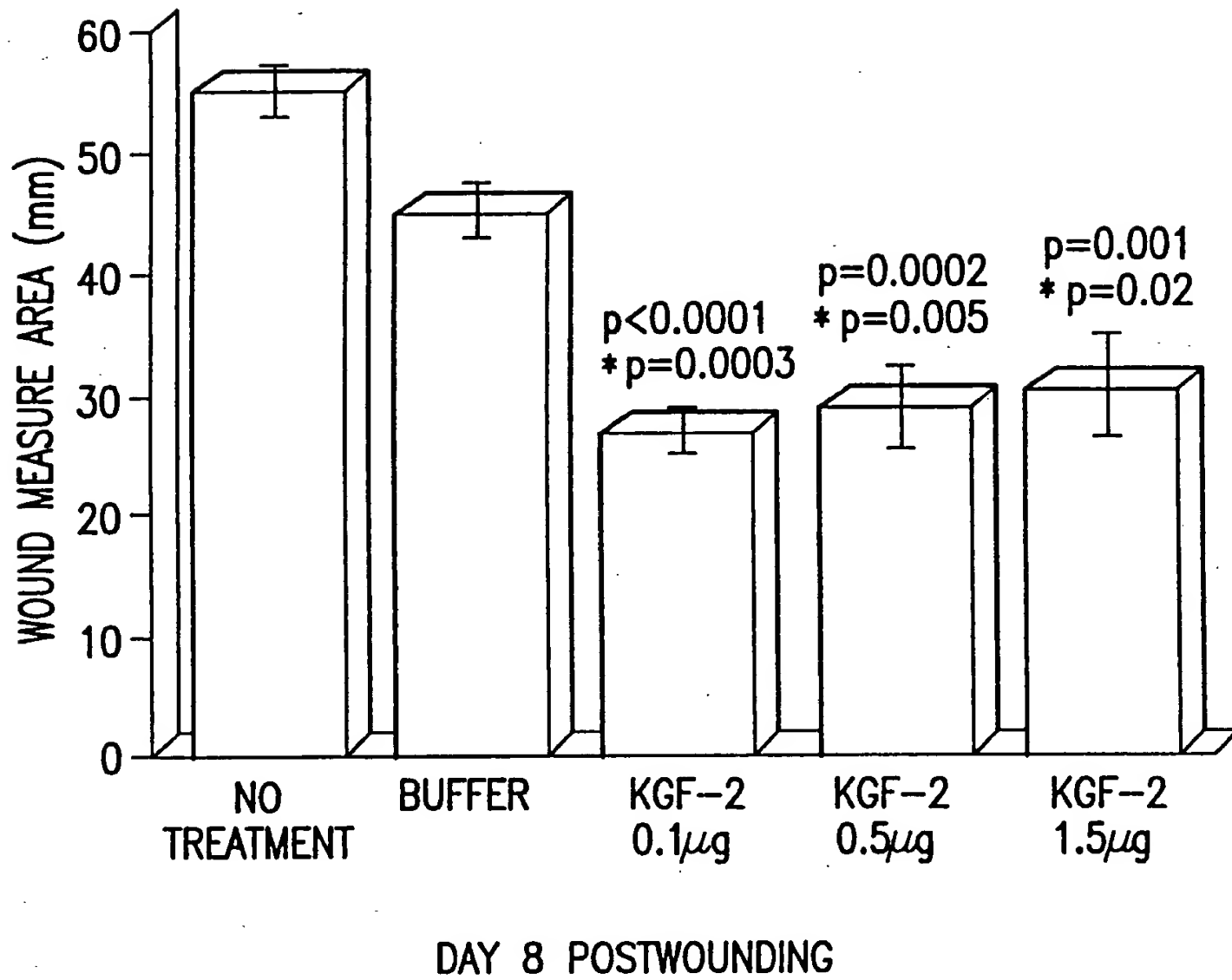


FIG.47

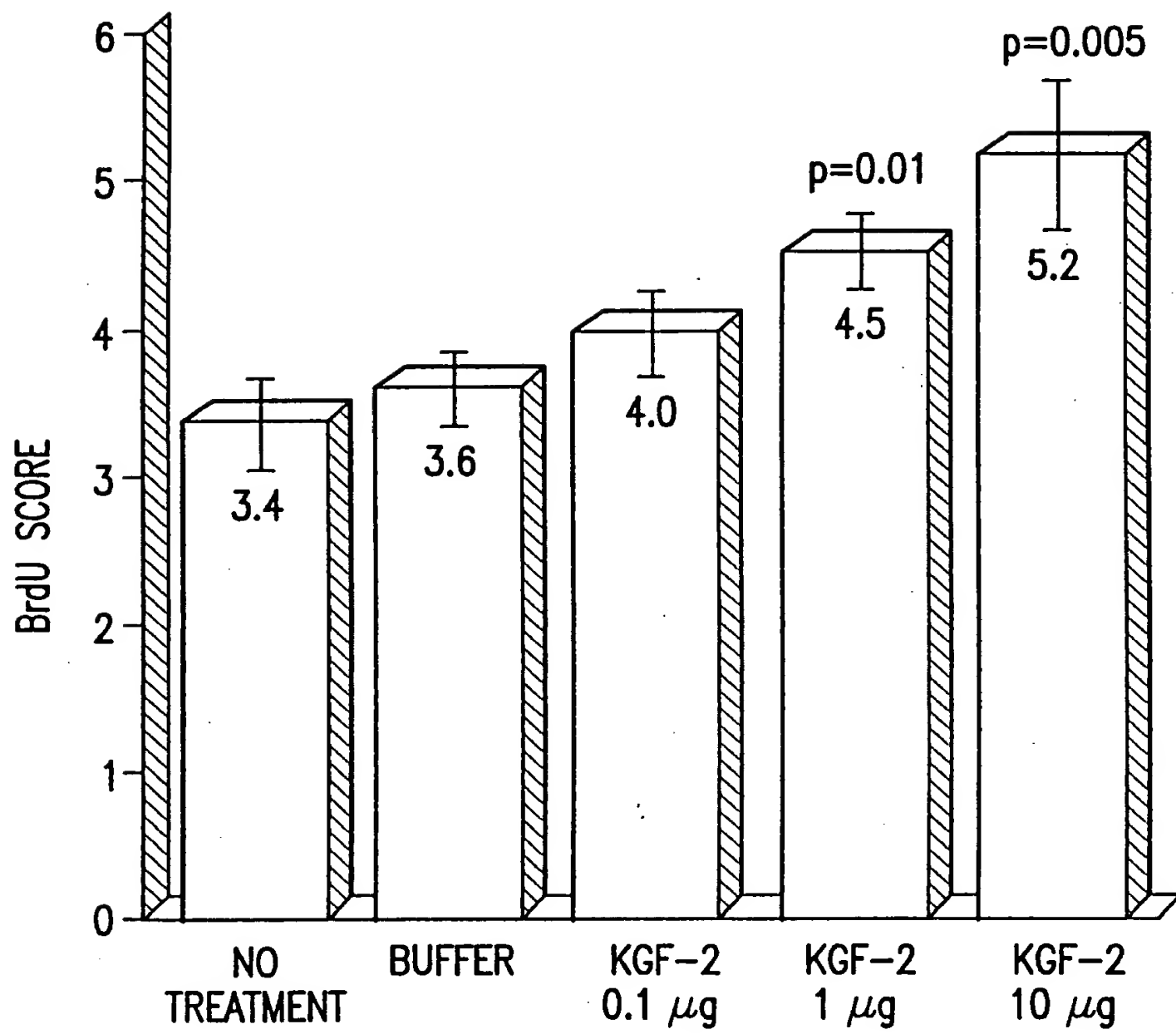


FIG.48

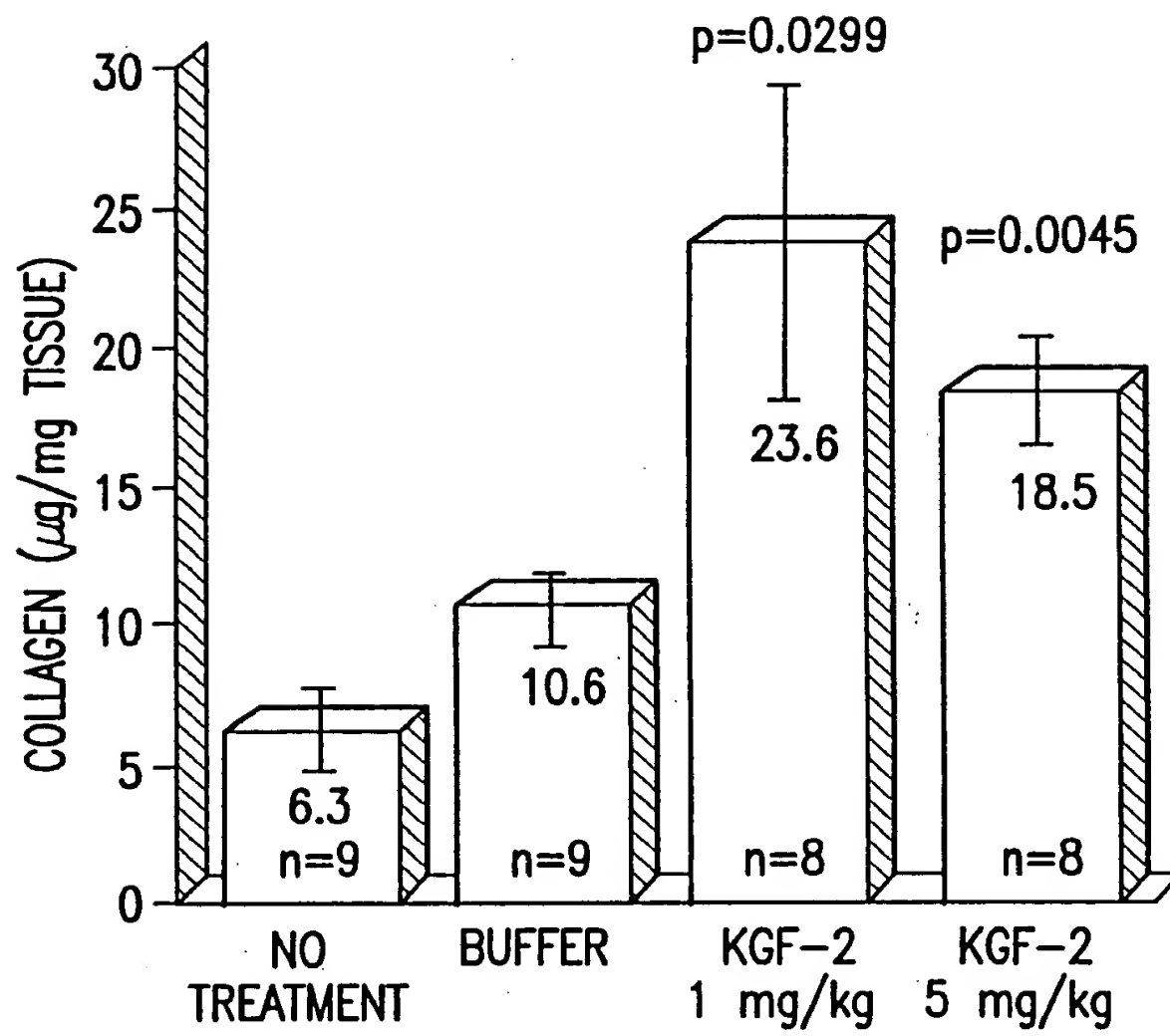


FIG.49

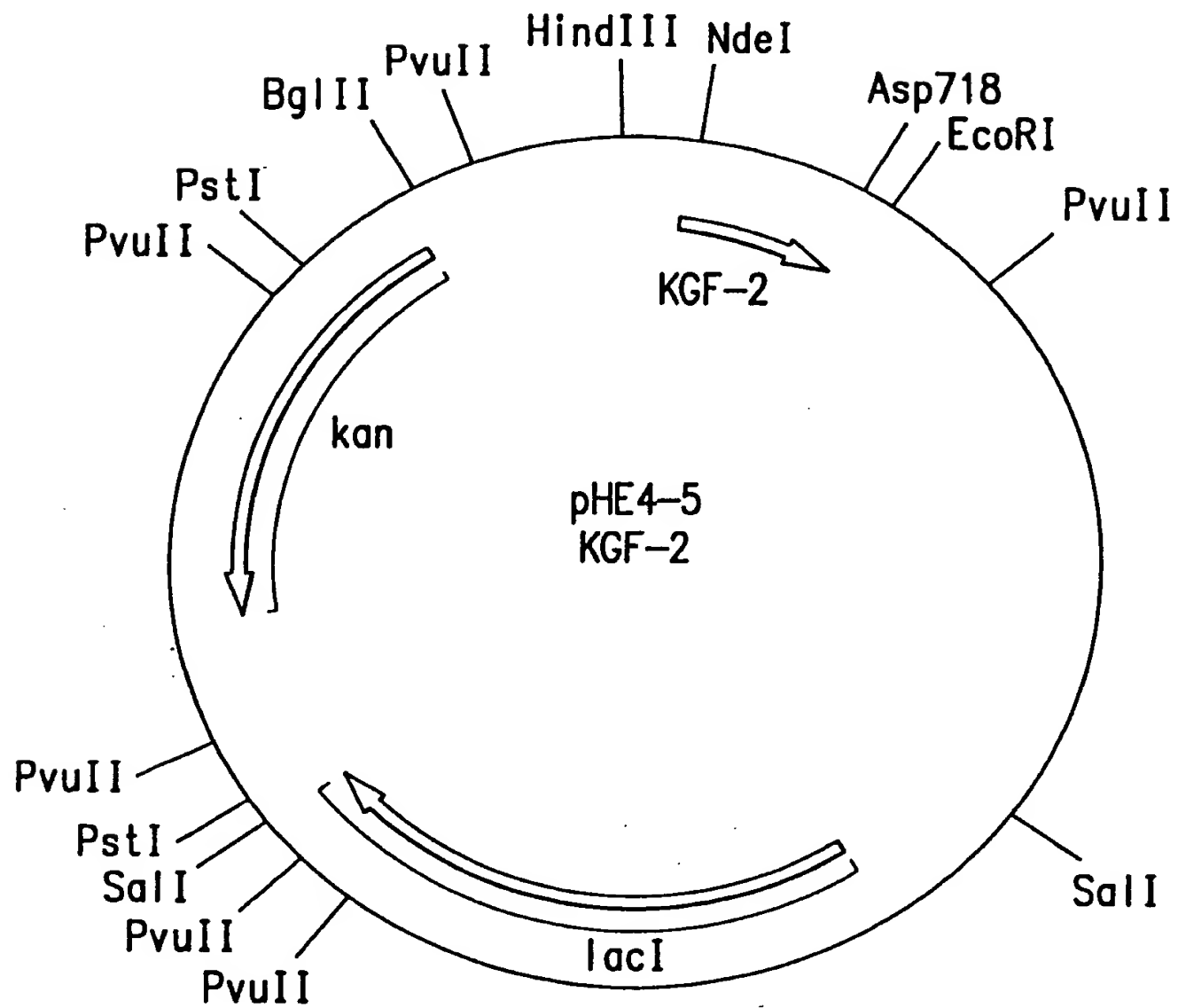


FIG. 50

1 AAGCTTAAAAAACTGCAAAAAATAGT ⁻³⁵ ^{Operator 1} TTGACT(TGTGAGCCGGATAACAAT)

50 ⁻¹⁰ TAAGATGTACCCA ^{Operator 2} ATTGTGAGCCGGATAACAATTCACACATTAA

94 ^{S/D} AGAGGAGAAATTA CATATG

FIG. 51

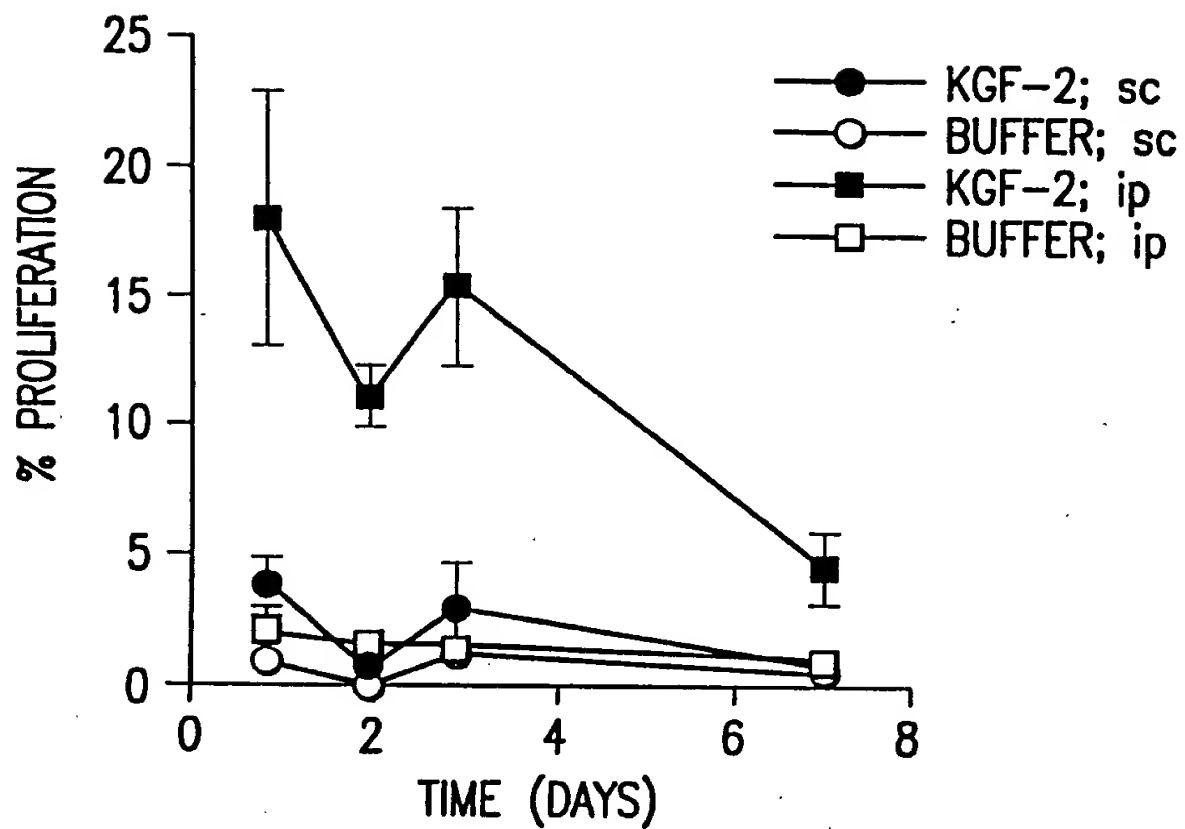


FIG. 52

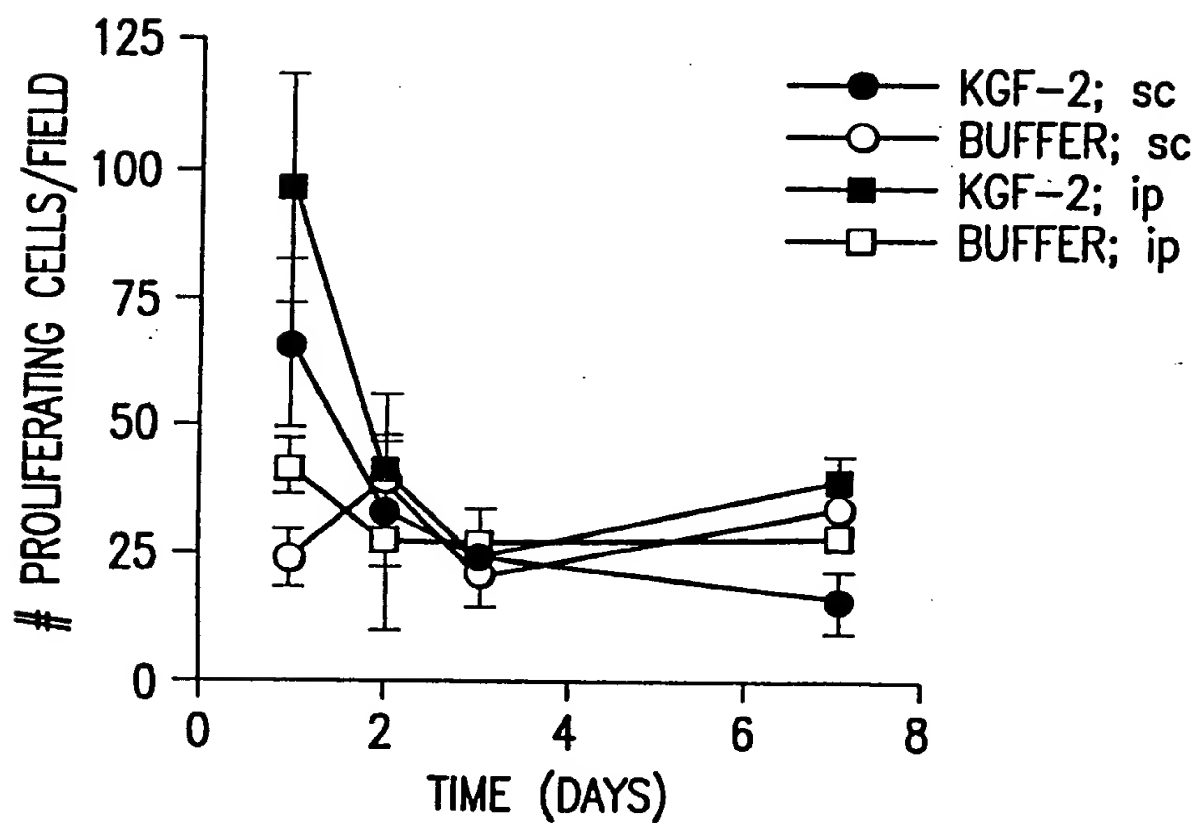


FIG. 53

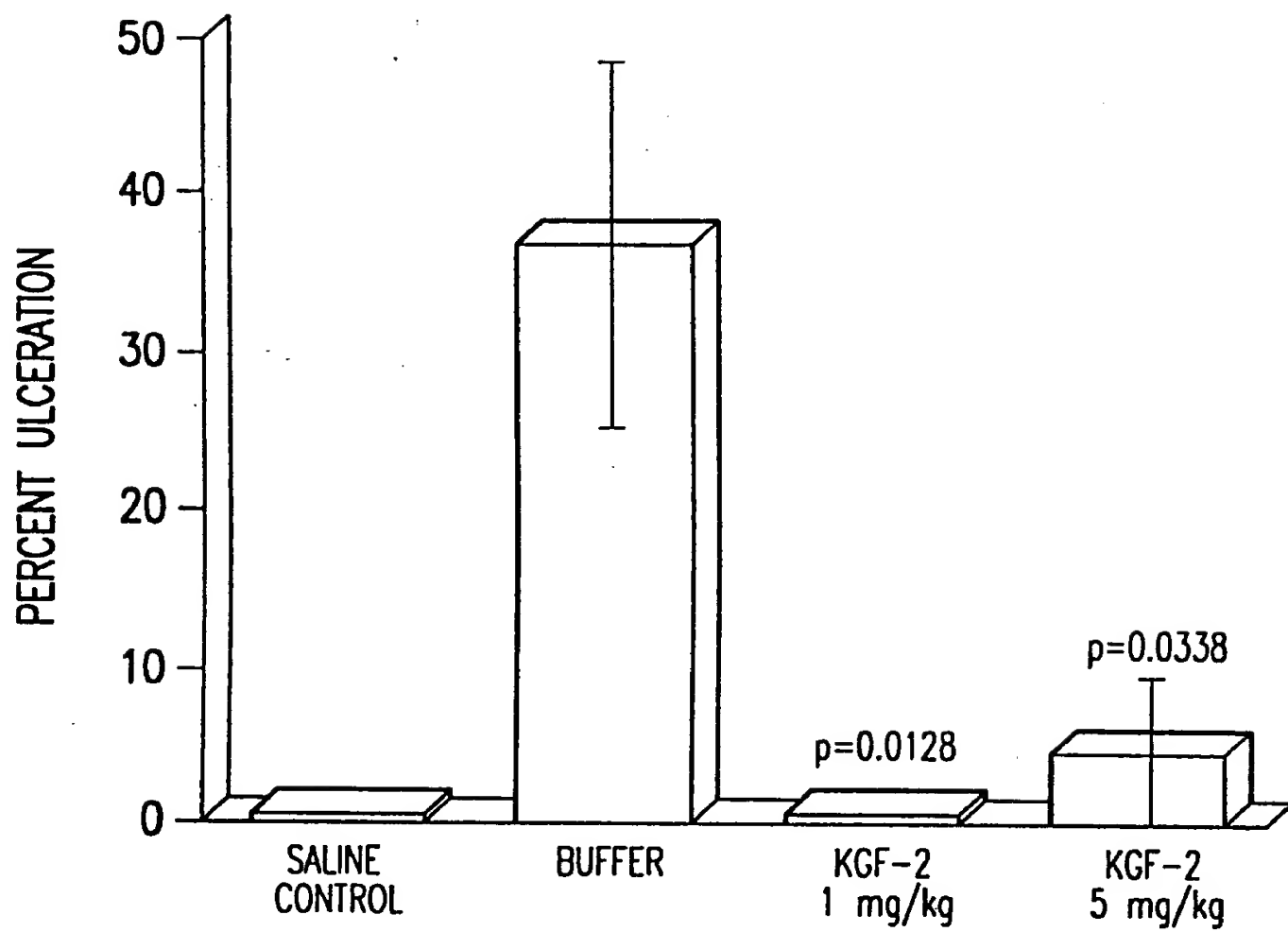


FIG. 54

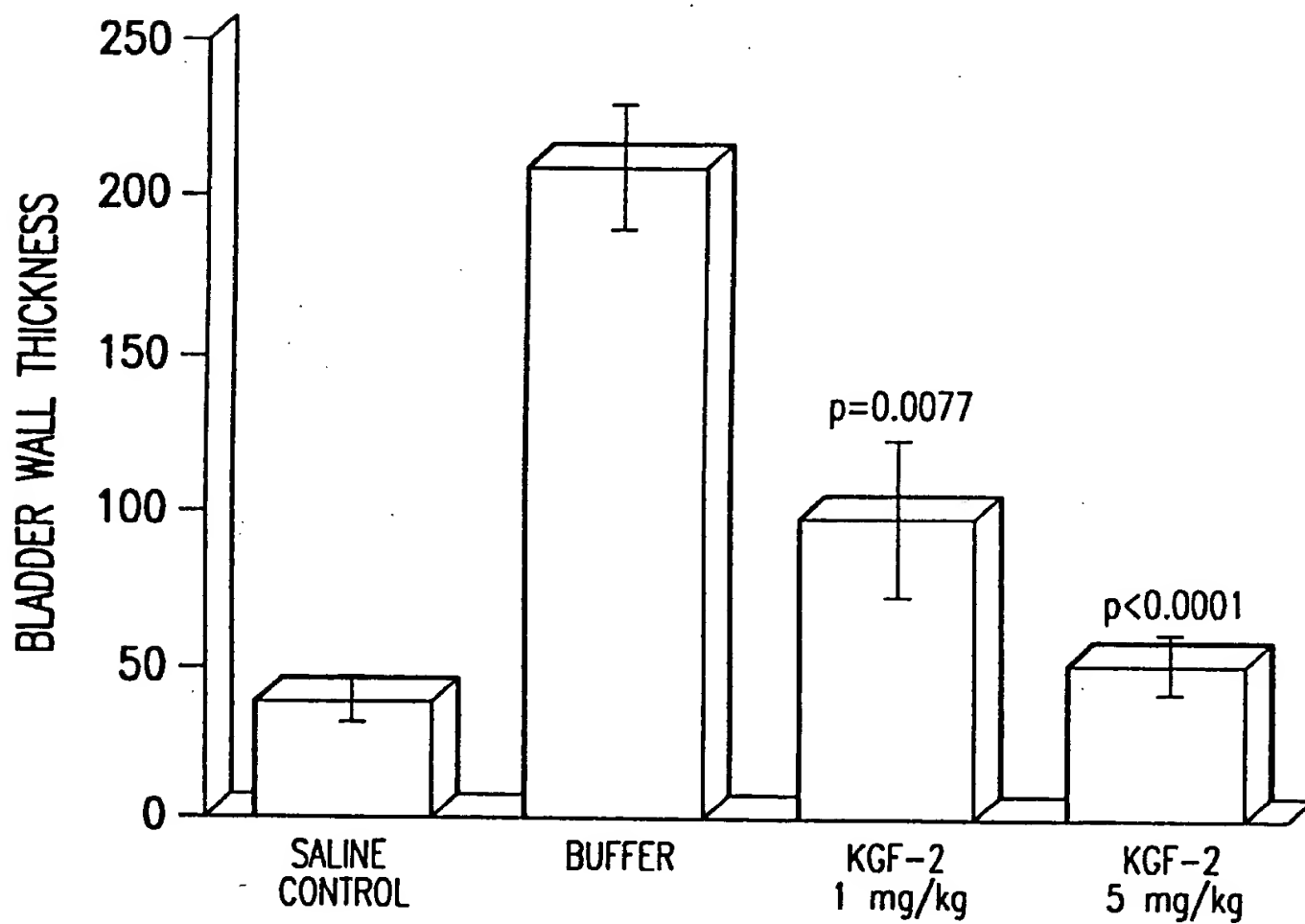


FIG. 55

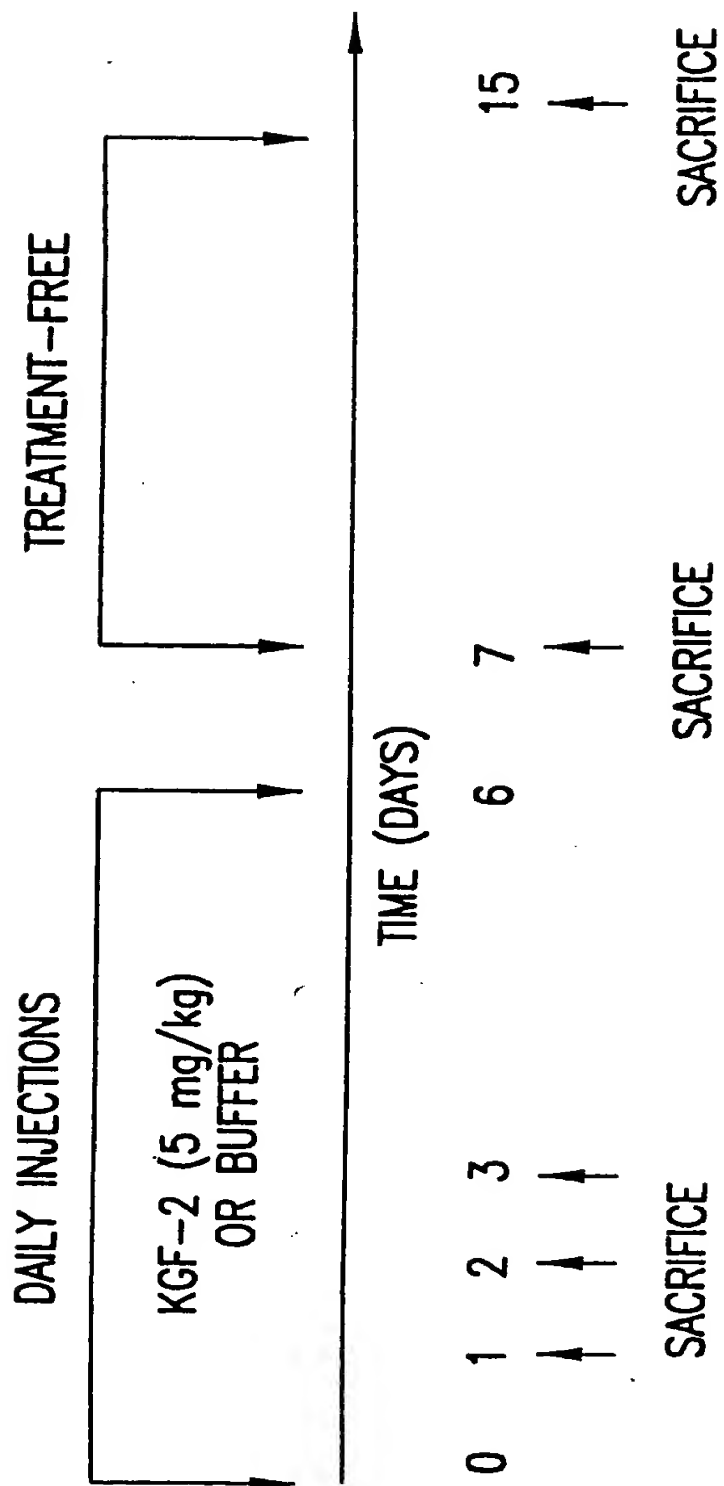


FIG. 56

PROLIFERATION OF HEPATOCYTES FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

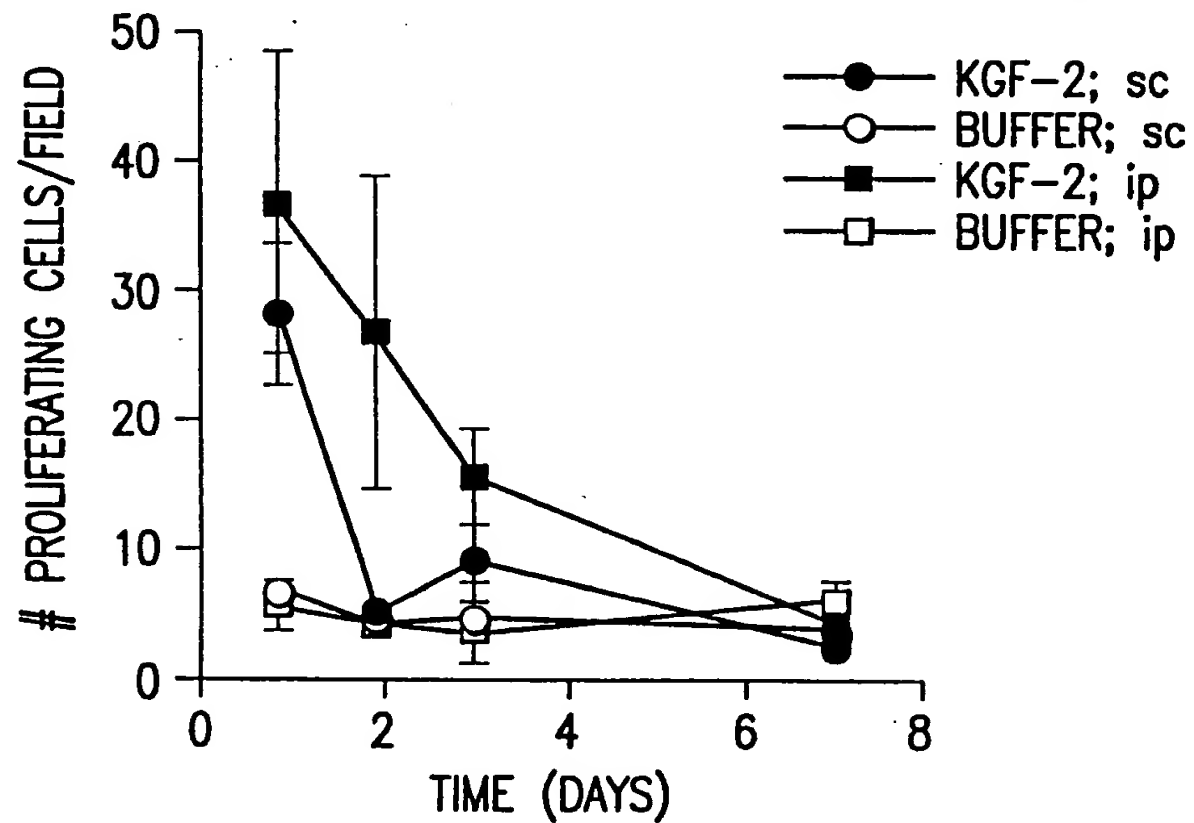


FIG. 57

PROLIFERATION OF PANCREATIC CELLS FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

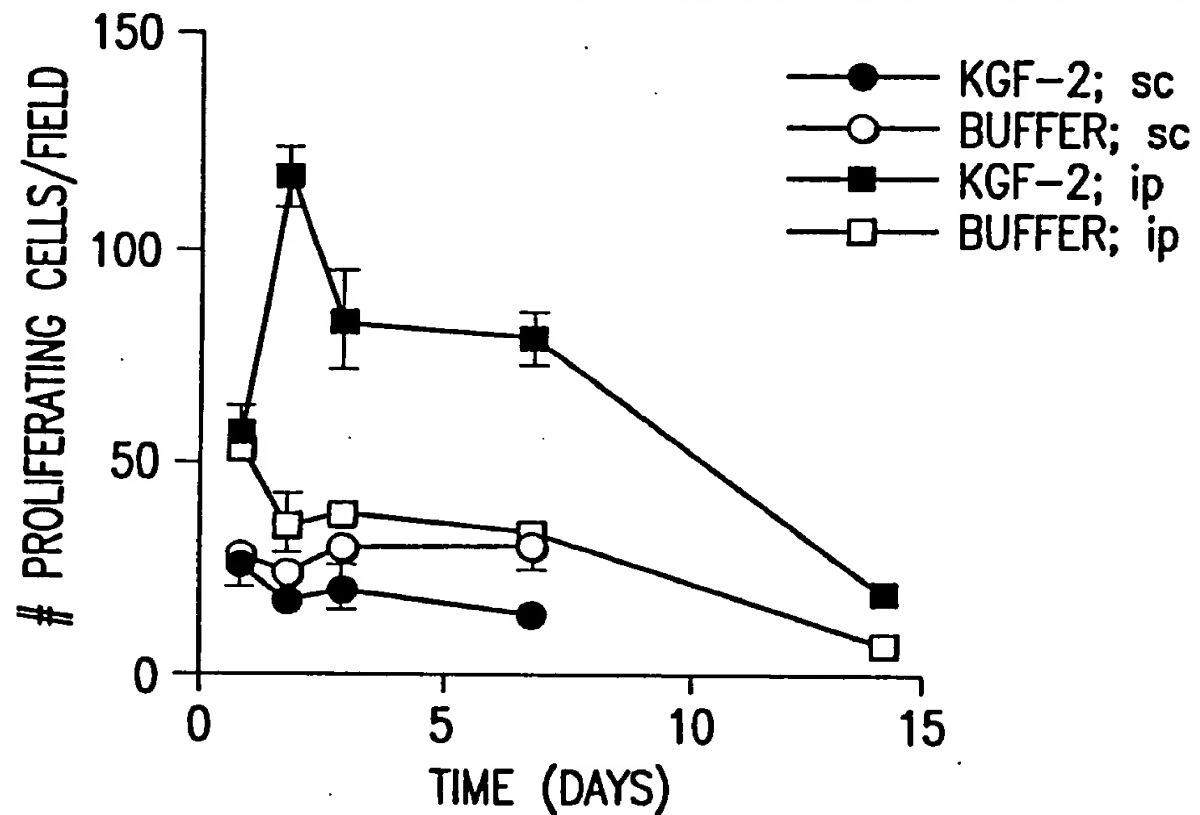


FIG. 58

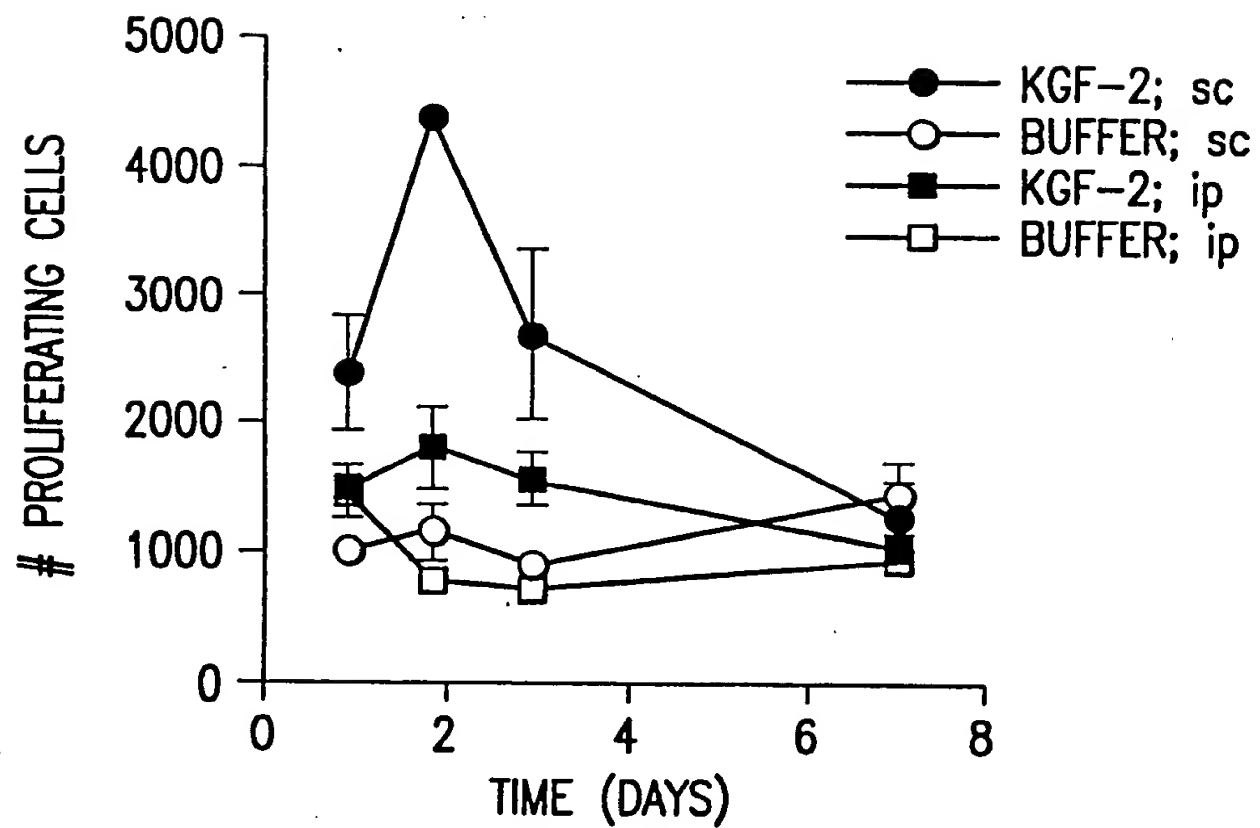


FIG. 59

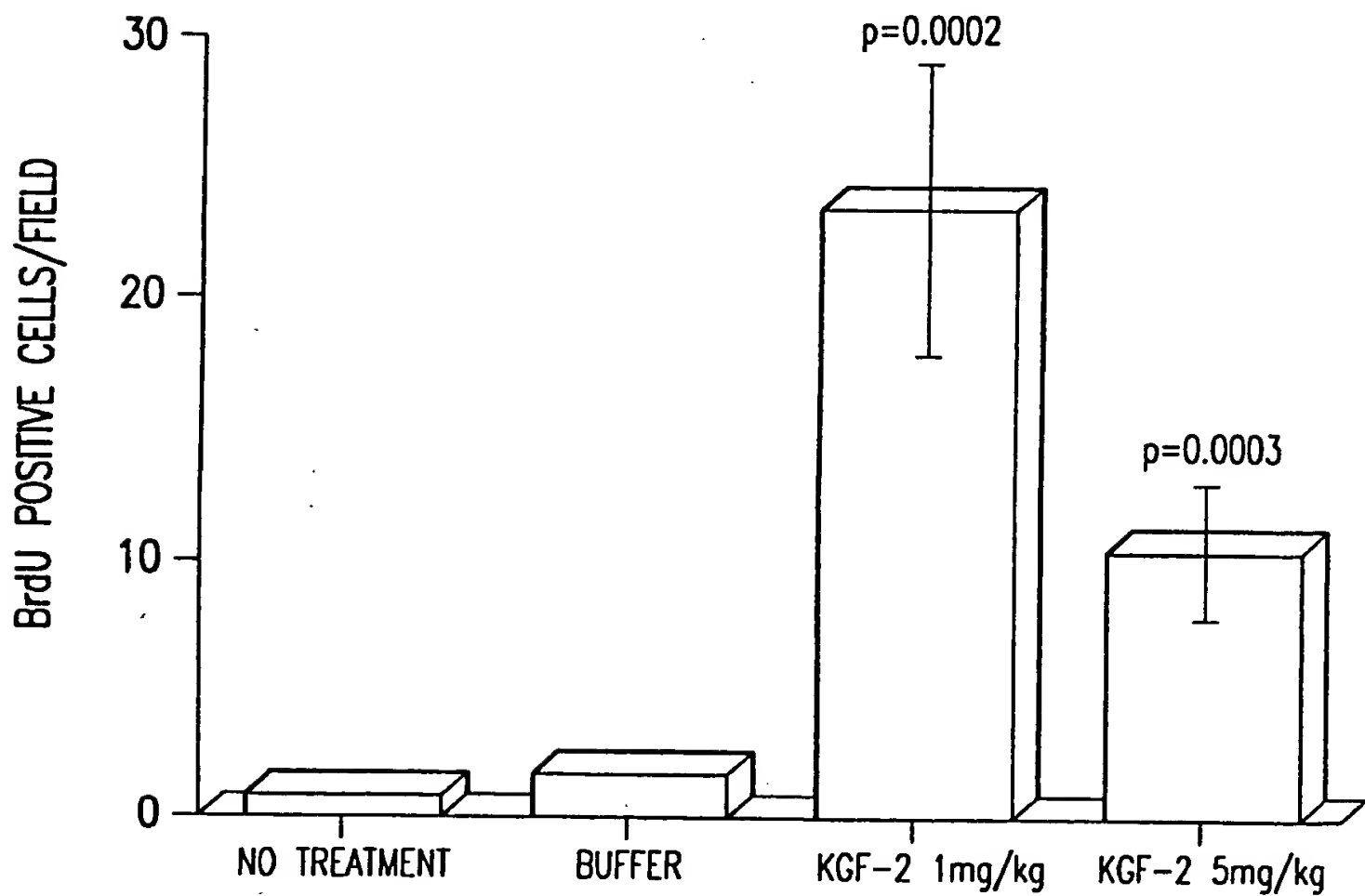


FIG. 60

**PThis Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☒ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.